#6

Figure 1

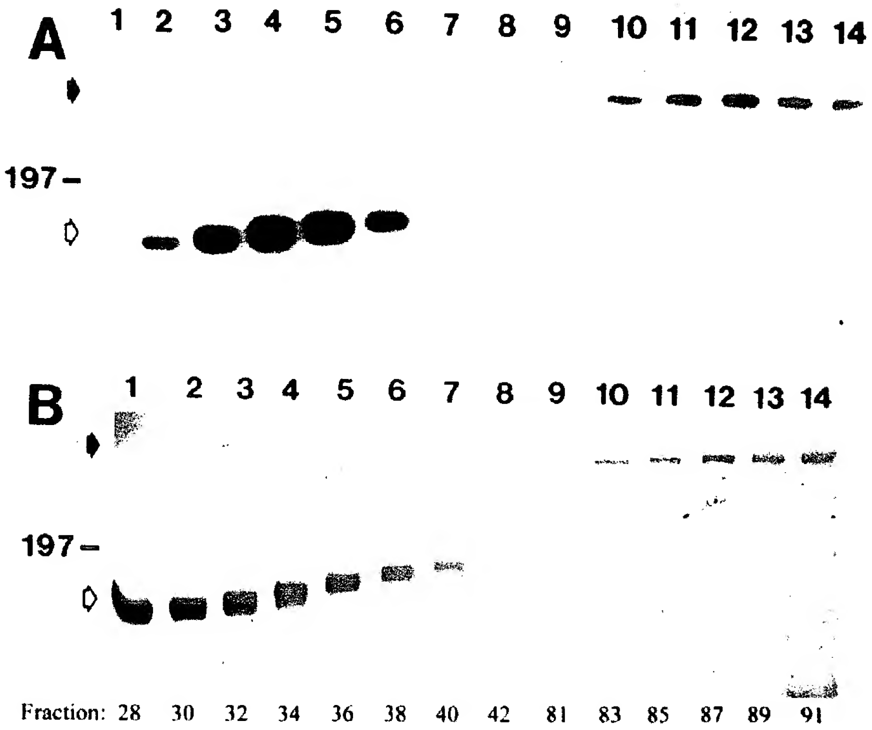

A
1 2 3 4 5 6 7 8 9 10 11 12 13 14
197–
B
1 2 3 4 5 6 7 8 9 10 11 12 13 14
197–
Fraction: 28 30 32 34 36 38 40 42 81 83 85 87 89 91

Figure 2

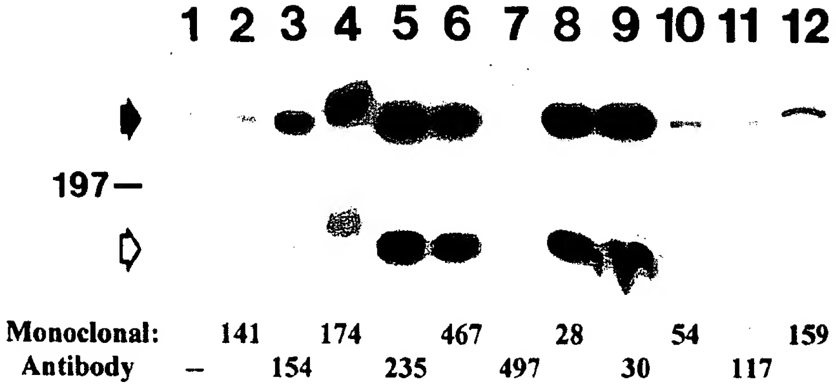

1 2 3 4 5 6 7 8 9 10 11 12
197—
Monoclonal: Antibody
–
141
154
174
235
467
497
28
30
54
117
159

Figure 3

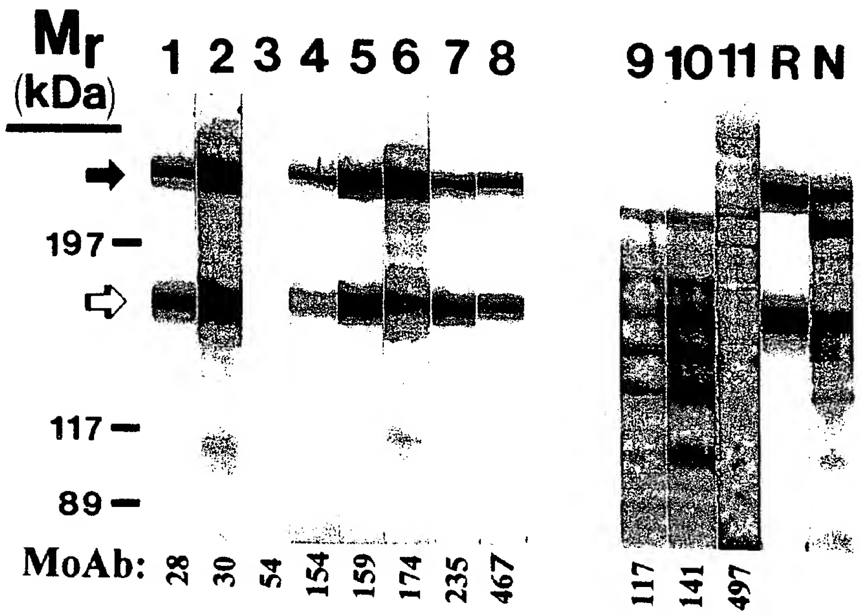

Mr
(kDa)
1 2 3 4 5 6 7 8
9 10 11 R N
197
117
89
MoAb:
28
30
54
154
159
174
235
467
117
141
497

Figure 4

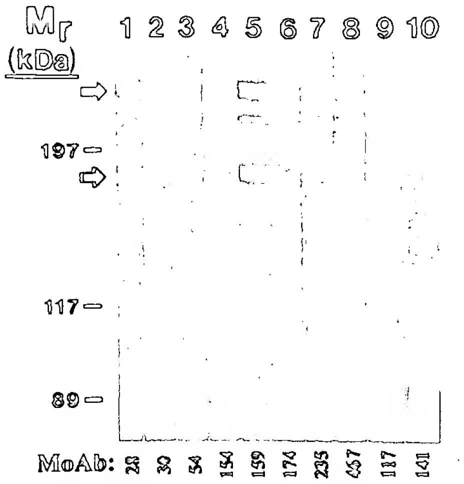

Mr
(kDa)
1 2 3 4 5 6 7 8 9 10
197
117
89
MoAb: 28 30 54 154 159 174 235 457 117 141

Figure 5

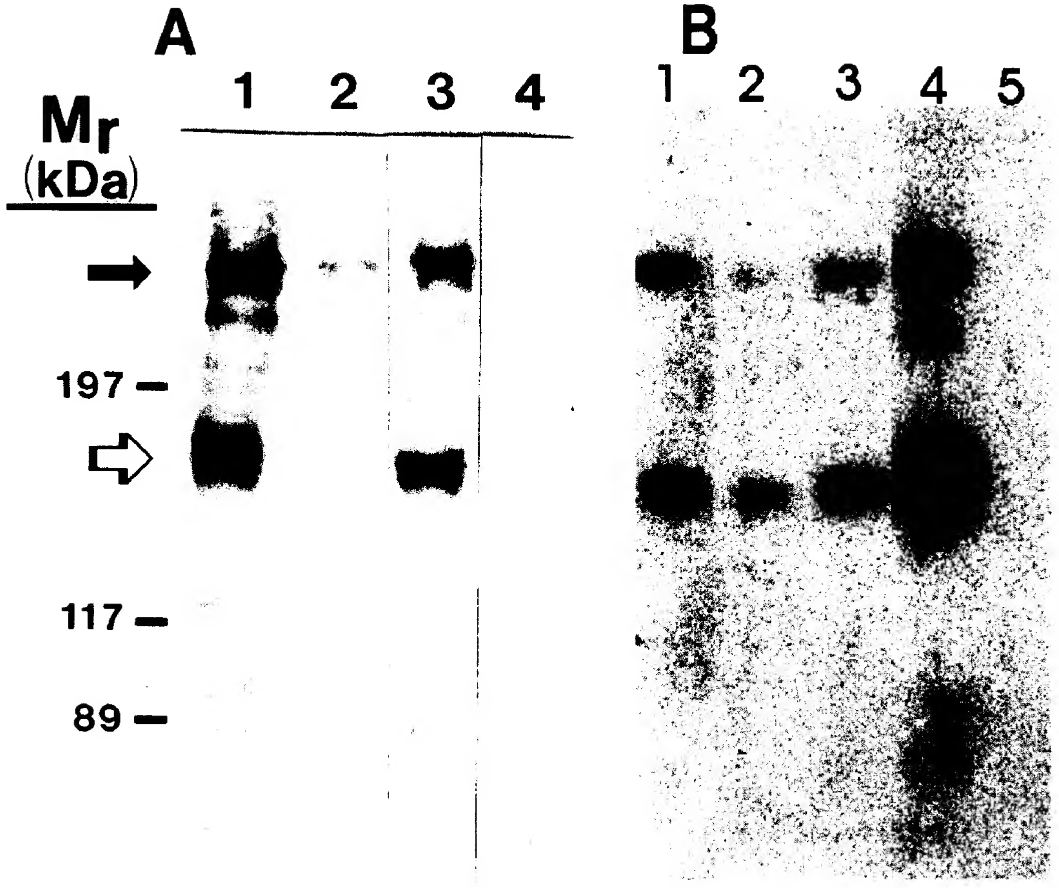
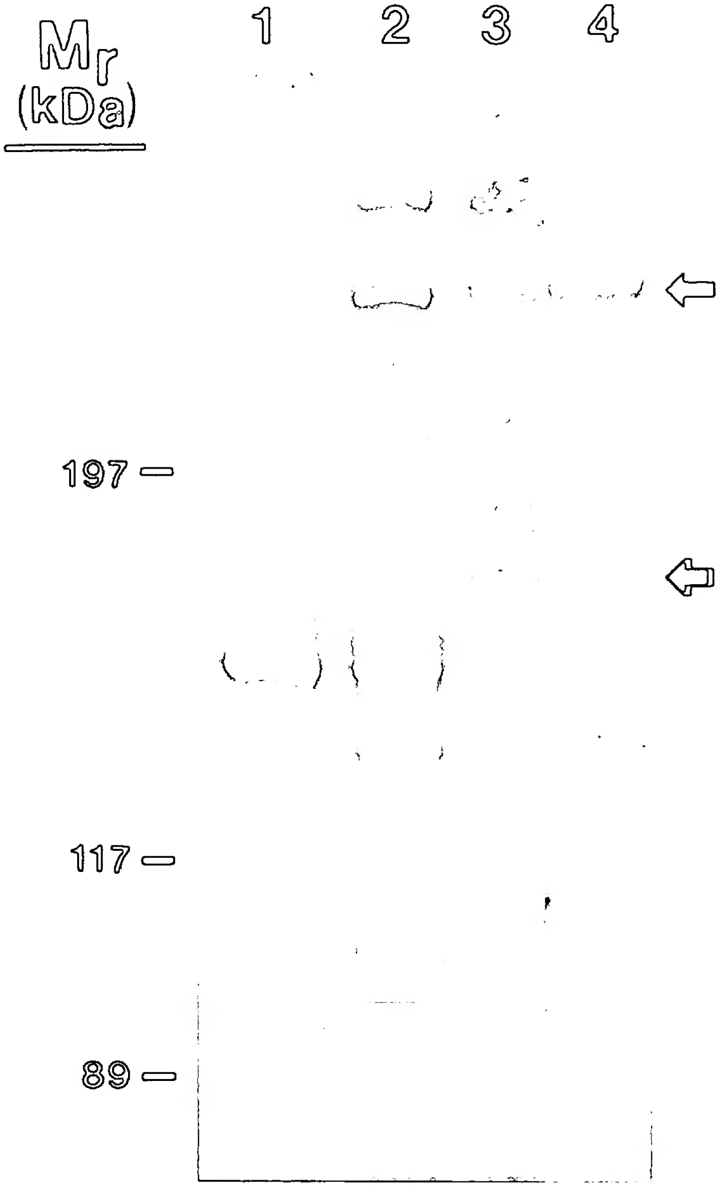

A
1
2
3
4
B
1
2
3
4
5
Mr (kDa)
197
117
89

Figure 6



M_r (kDa)
1
2
3
4
197
117
89

Figure 7

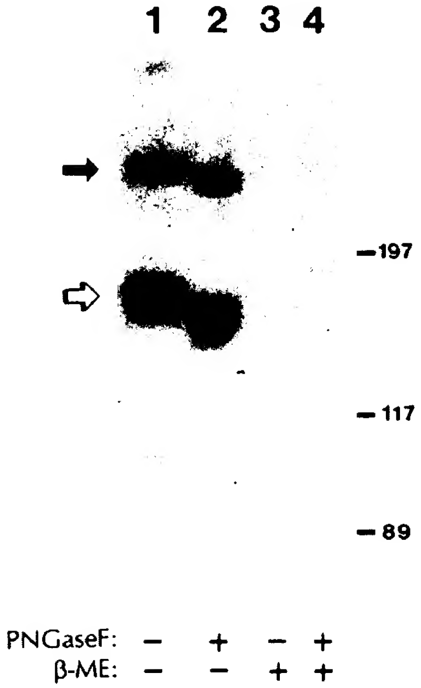
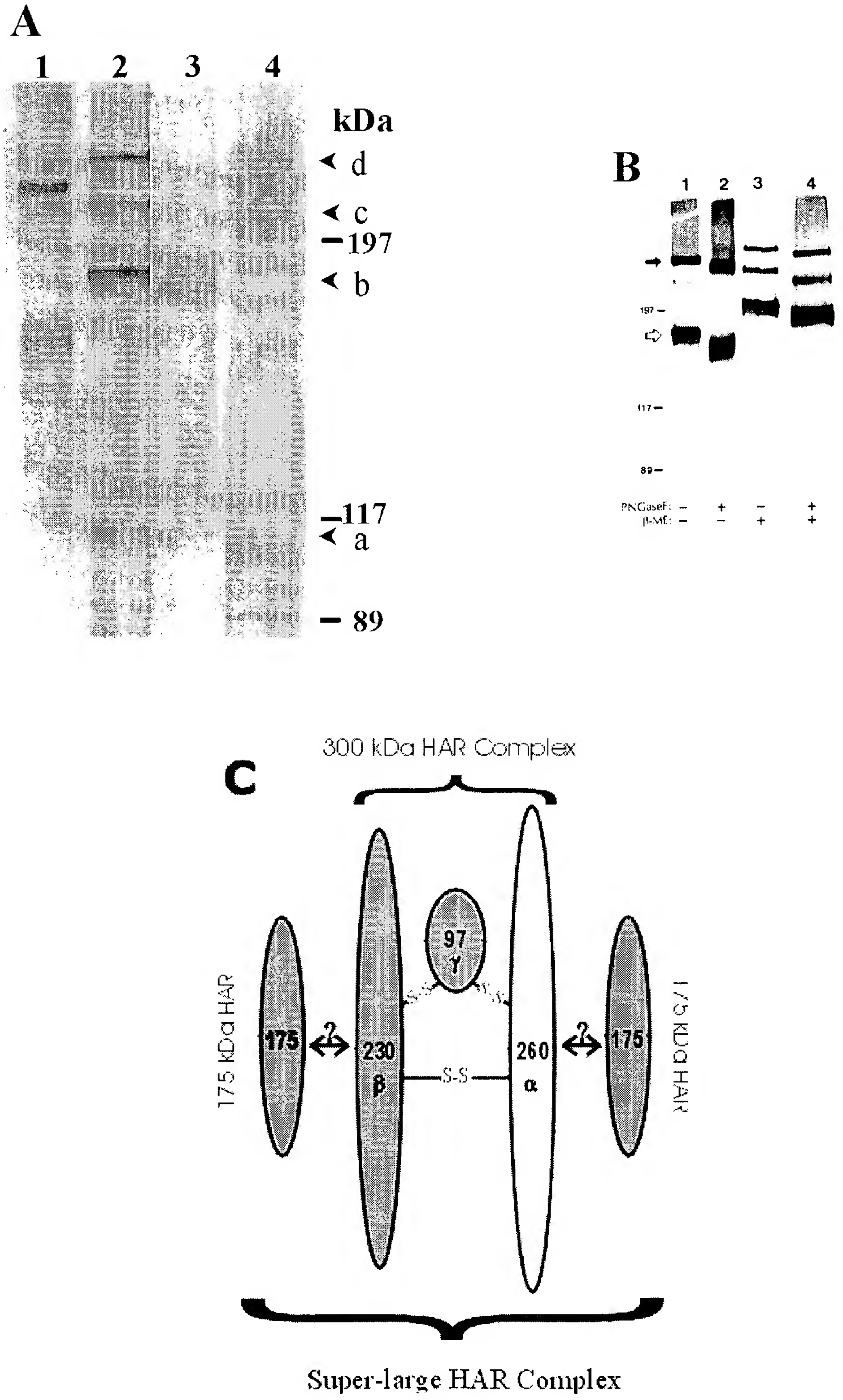

1
2
3
4
197
117
89
PNGaseF: − + − +
β-ME: − − + +

Figure 8


A
1
2
3
4
kDa
d
c
197
b
117
a
89
B
1
2
3
4
197
117
89
PNGaseF: − + − +
β-ME: − − + +
C
300 kDa HAR Complex
175 kDa HAR
175
230
β
97
γ
S-S
S-S
S-S
260
α
175
175 kDa HAR
Super-large HAR Complex

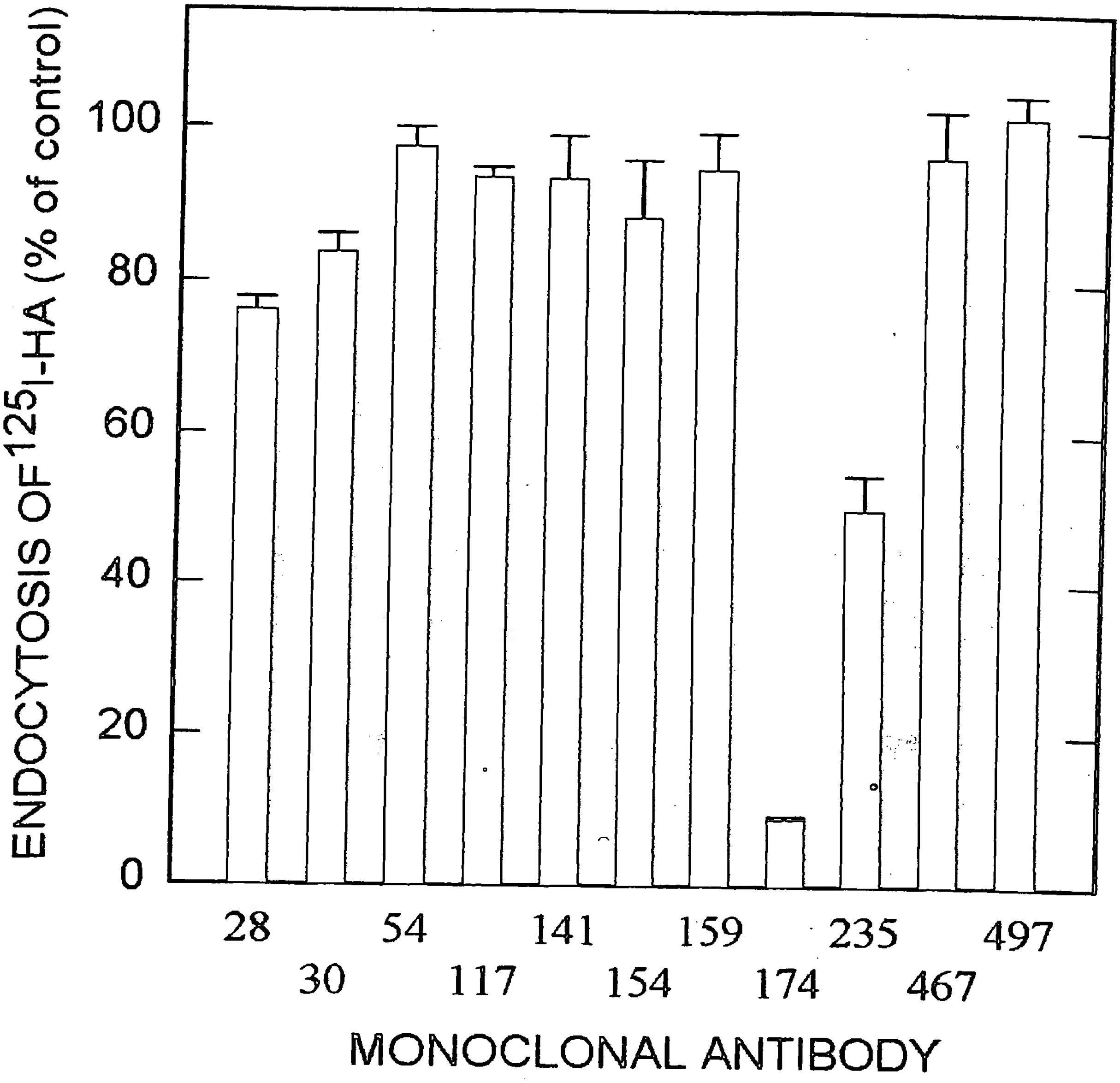

ENDOCYTOSIS OF ^{125}I-HA (% of control)
100
80
60
40
20
0
28
30
54
117
141
154
159
174
235
467
497
MONOCLONAL ANTIBODY

Figure 9

Figure 10

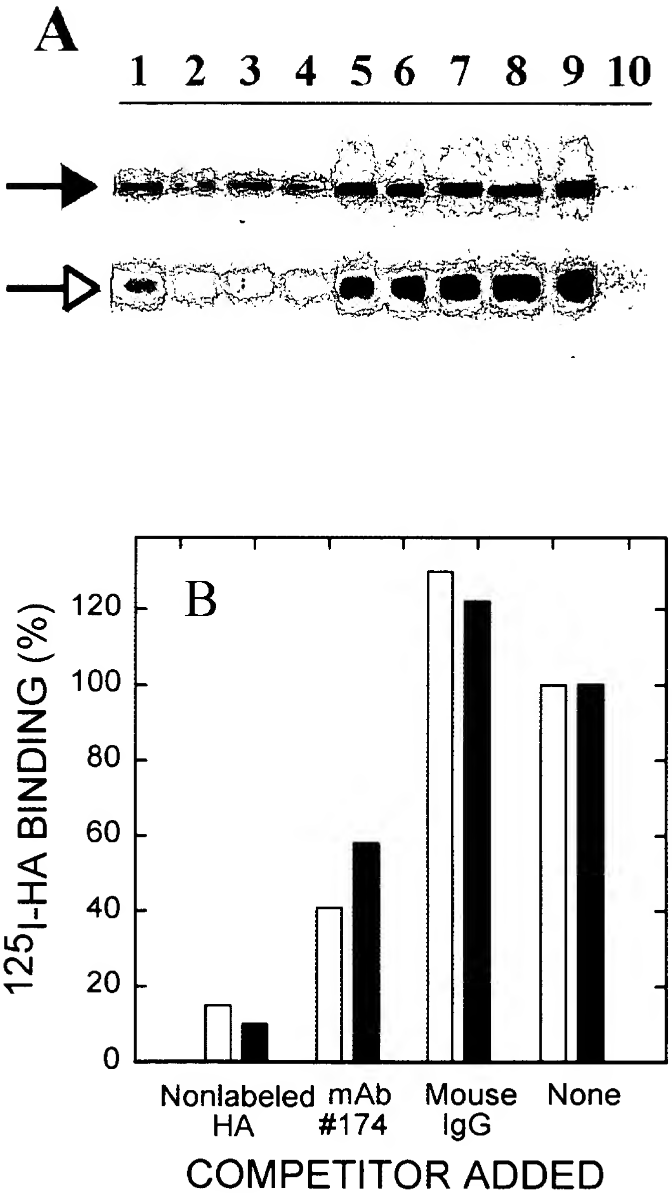

A
1
2
3
4
5
6
7
8
9
10
B
125I-HA BINDING (%)
0
20
40
60
80
100
120
Nonlabeled HA
mAb #174
Mouse IgG
None
COMPETITOR ADDED

Figure 11

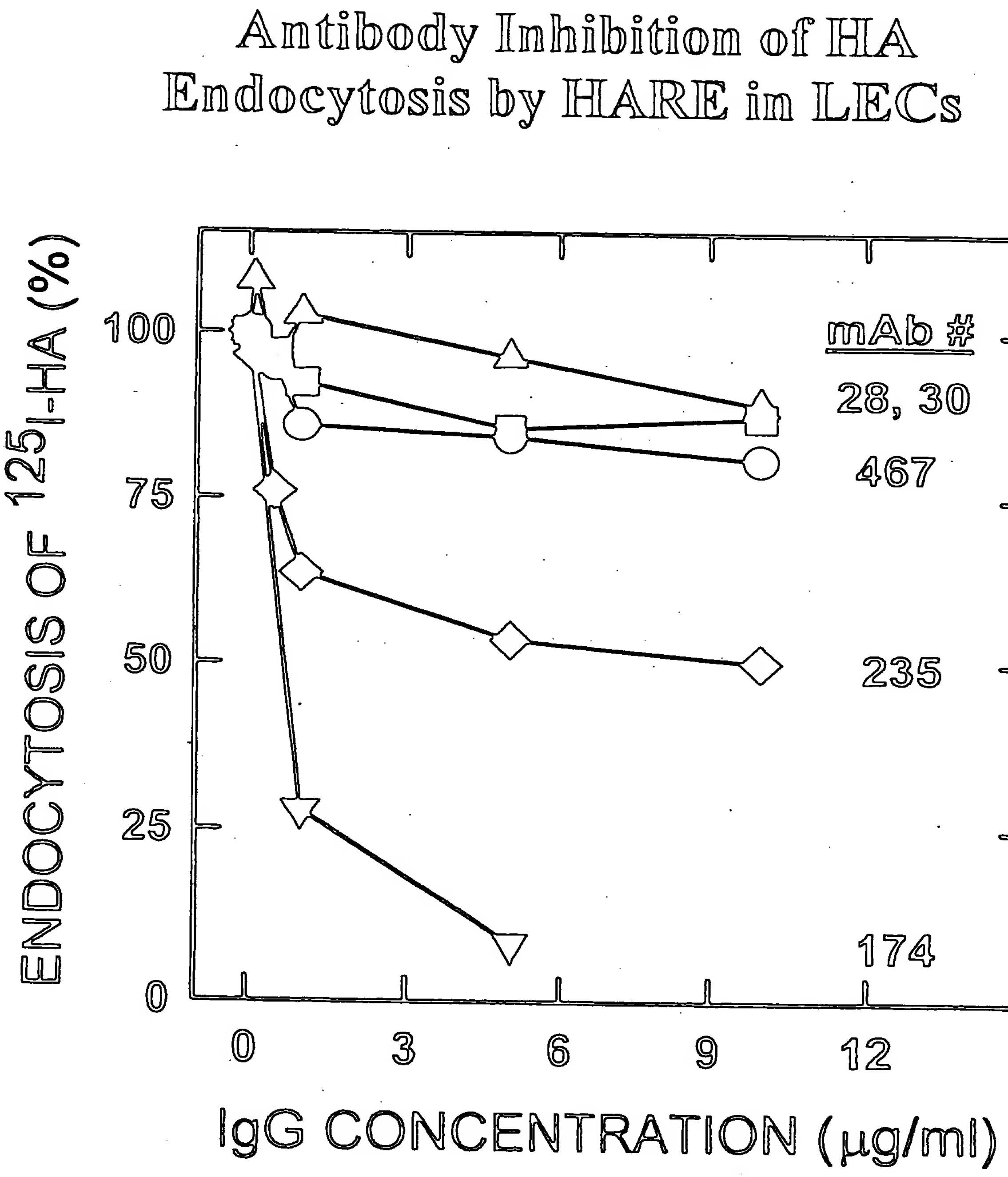

Antibody Inhibition of HA Endocytosis by HARE in LECs
ENDOCYTOSIS OF ^{125}I-HA (%)
100
75
50
25
0
0
3
6
9
12
IgG CONCENTRATION (μg/ml)
mAb #
28, 30
467
235
174

Figure 12

Antibody Inhibition of HA Binding to HARE on LECs is Temperature Dependent

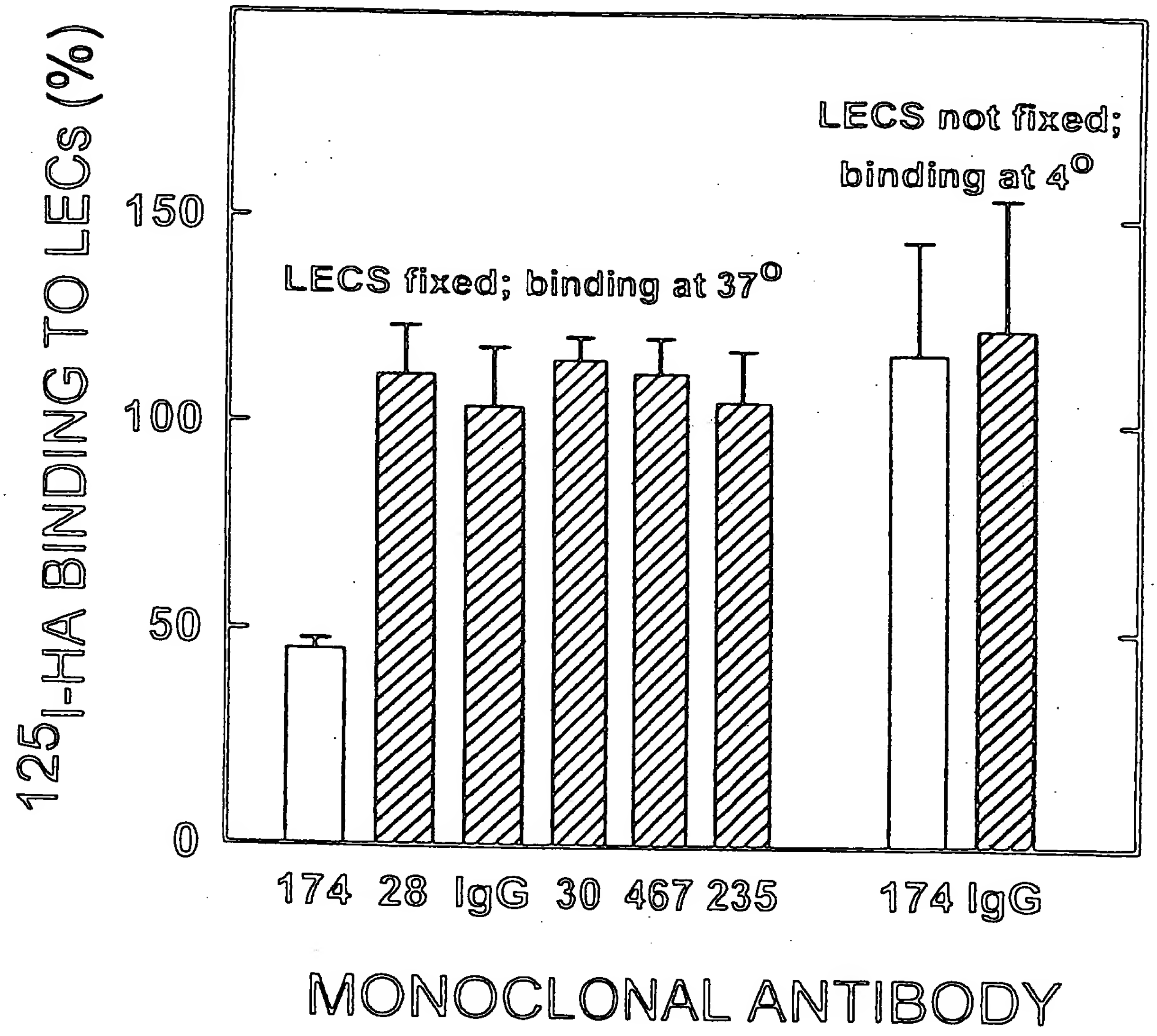


Figure 13

Figure 13

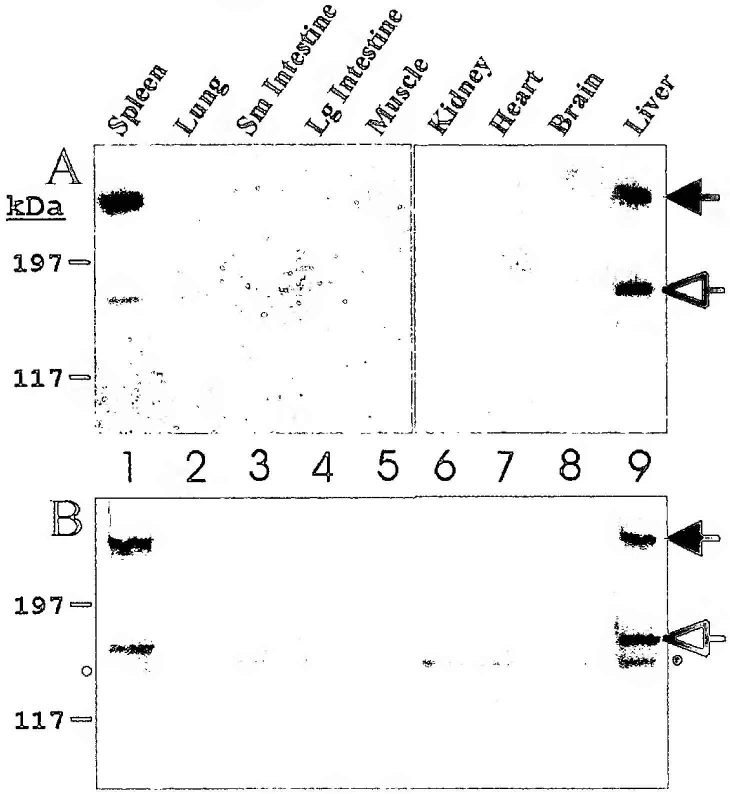
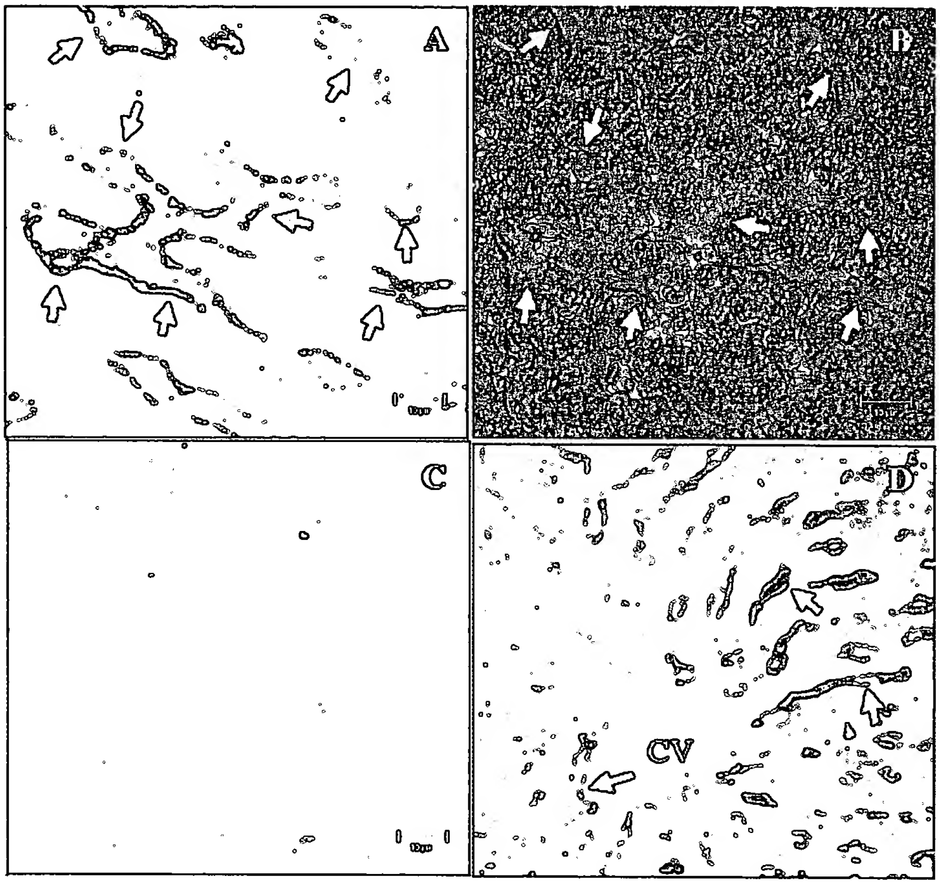

Spleen
Lung
Sm Intestine
Lg Intestine
Muscle
Kidney
Heart
Brain
Liver
A
kDa
197
117
1
2
3
4
5
6
7
8
9
B
197
117

Figure 14



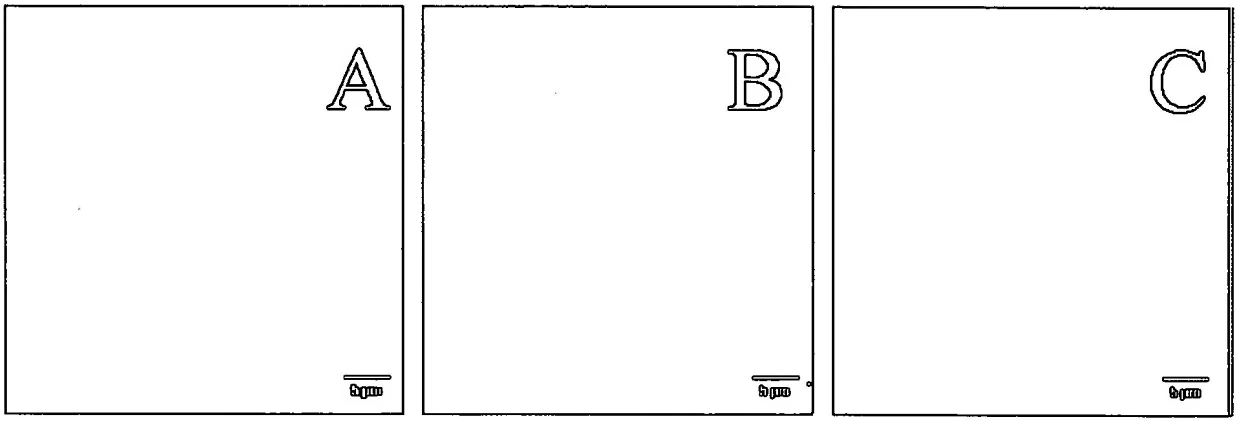
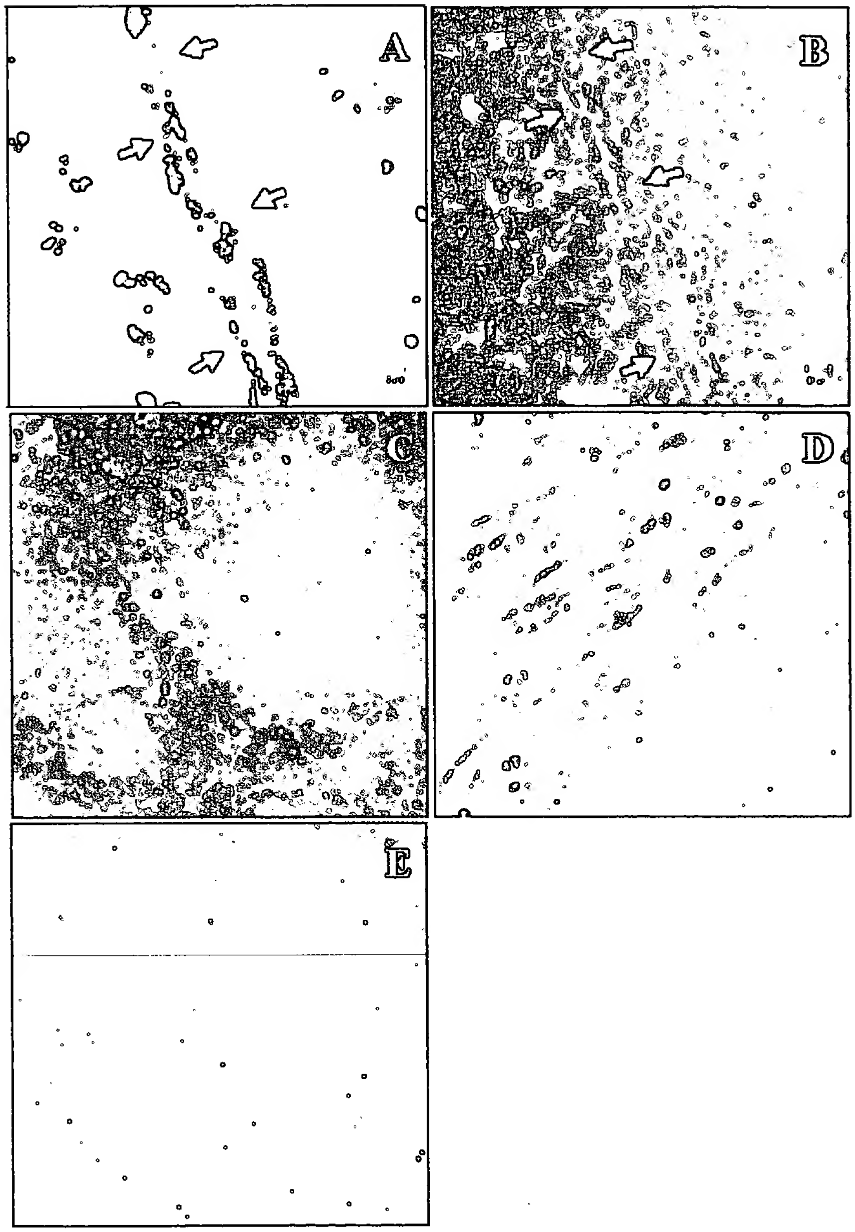

A
5µm
B
5µm
C
5µm

Figure 15

Figure 16



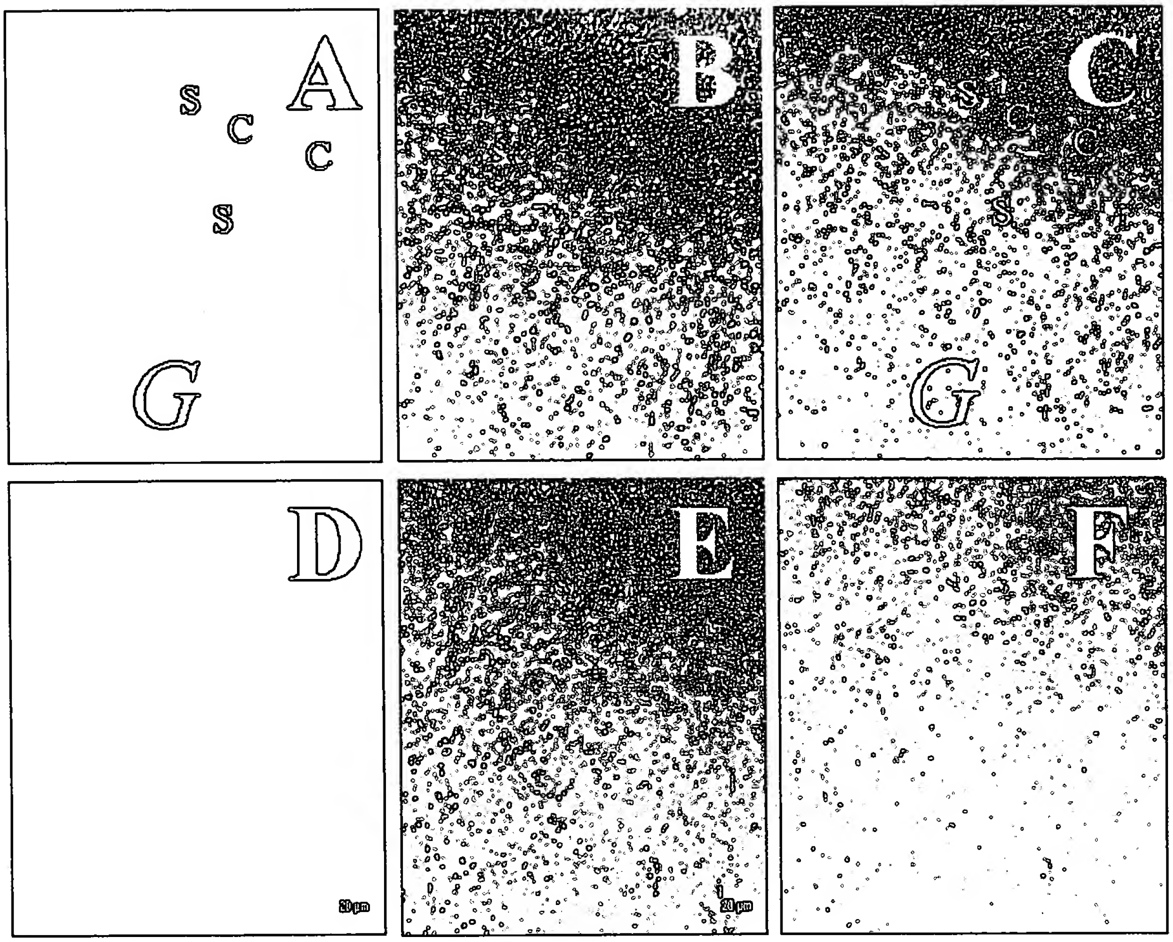
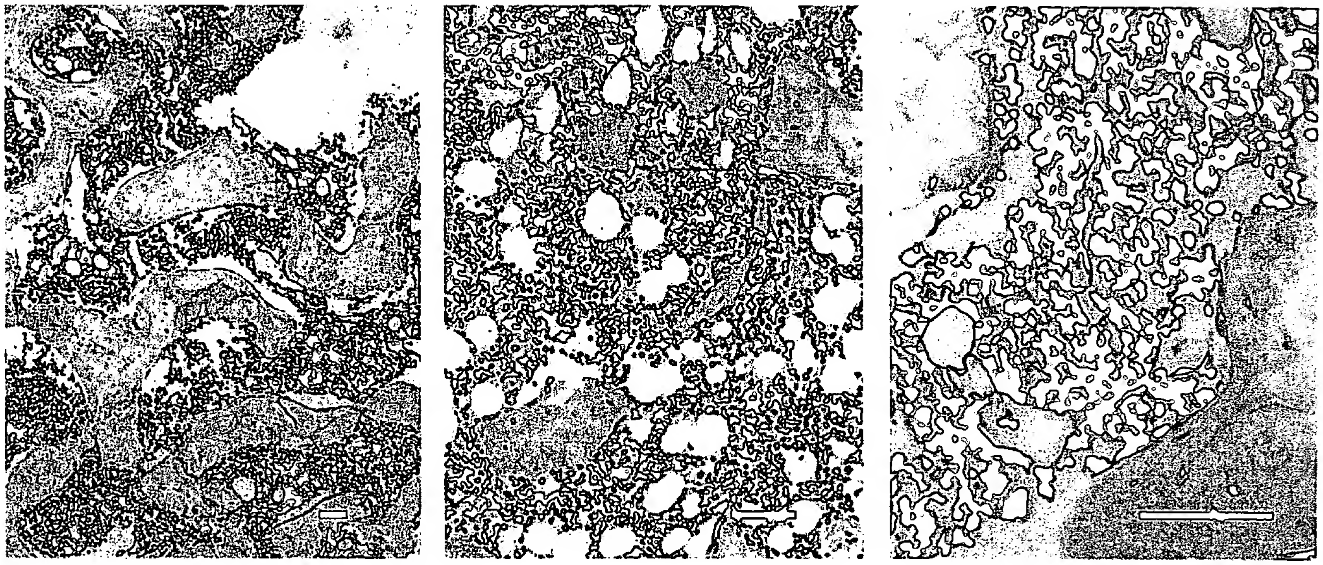

A
s
c
c
s
G
B
C
s
c
c
s
G
D
20 µm
E
20 µm
F

Figure 17

Figure 18

Immunolocalization of HARE in Bone Marrow



Control

Bars = 50 um

Figure 19

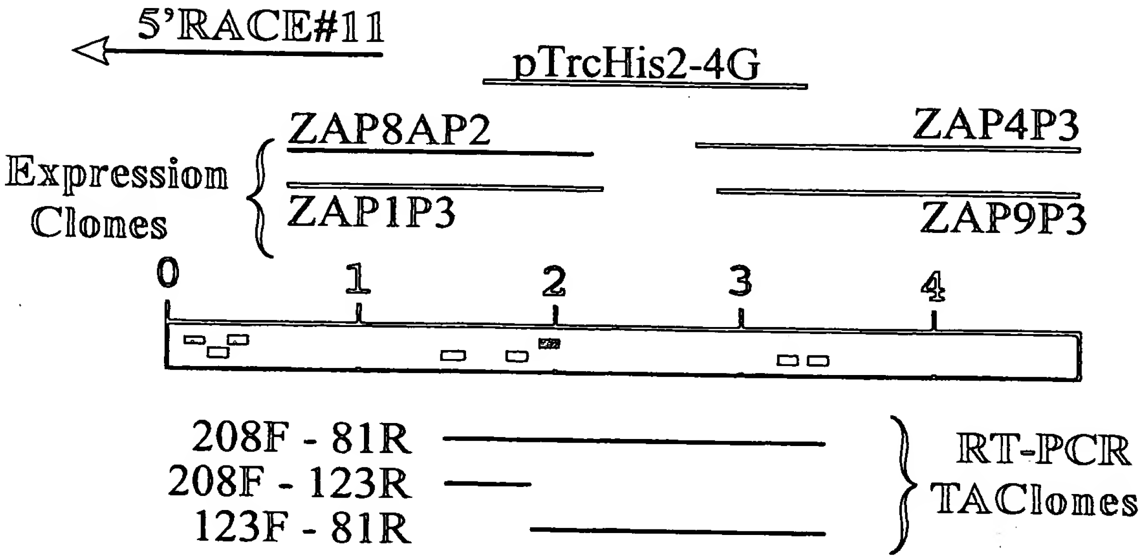

5'RACE#11
pTrcHis2-4G
Expression Clones
ZAP8AP2
ZAP1P3
ZAP4P3
ZAP9P3
0
1
2
3
4
208F - 81R
208F - 123R
123F - 81R
RT-PCR TAClones

Figure 20

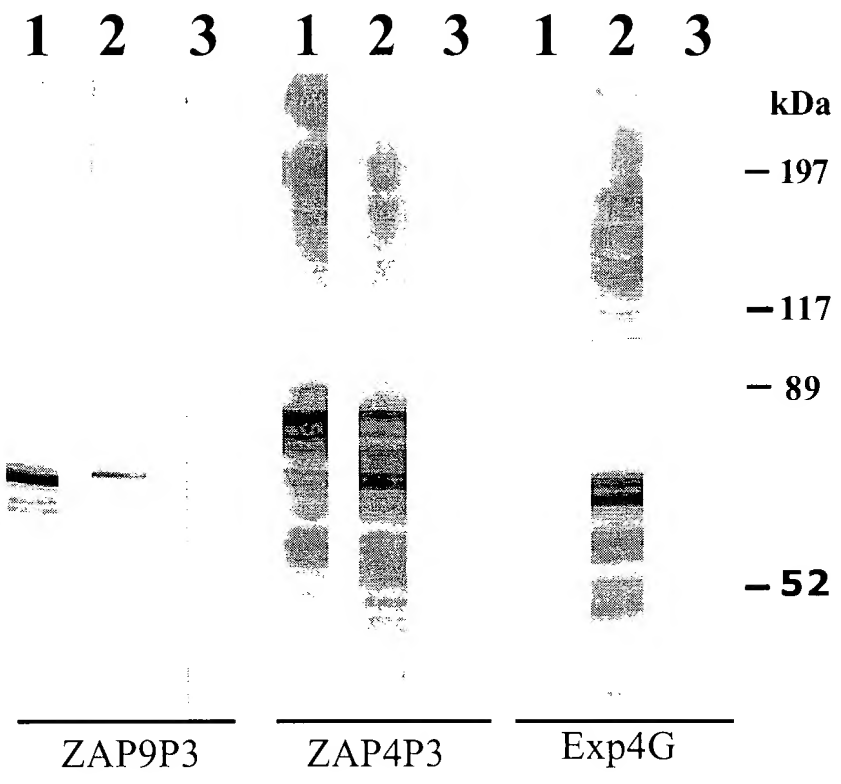

1
2
3
1
2
3
1
2
3
kDa
197
117
89
52
ZAP9P3
ZAP4P3
Exp4G

Figure 21

```
   1 TCTTTACCAAGTCTACTCACCCGTCTGGAGCAGATGCCCGACTATTCCATTTTCCGAGGTTACATTATTCATTACAACCTGGCAAGTGCAATCGAGTCTGCAGATGCTTATACTGTGTTC
   1 S  L  P  S  L  L  T  R  L  E  Q  M  P  D  Y  S  I  F  R  G  Y  I  I  H  Y  N  L  A  S  A  I  E  S  A  D  A  Y  T  V  F
 121 GTGCCAAACAATGAAGCCATCGAAAACTATATCAGGGAGAAGAAAGCCACATCTCTAAAGGAAGATATTCTACGGTACCATGTGGTCCTGGGGGAAAAGCTCCTGAAGAATGACTTGCAT
  41 V  P  N  N  E  A  I  E  N  Y  I  R  E  K  K  A  T  S  L  K  E  D  I  L  R  Y  H  V  V  L  G  E  K  L  L  K  N  D  L  H
 241 AACGGCATGCACCGAGAGACCATGCTGGGGTTCTCCTACCTCCTTGCCTTCTTTCTCCGCAATGACCAGCTGTATGTAAATGAAGCTCCAATAAACTACACCAATGTGGCCACTGATAAA
  81 N  G  M  H  R  E  T  M  L  G  F  S  Y  L  L  A  F  F  L  R  N  D  Q  L  Y  V  N  E  A  P  I  N  Y  T  N  V  A  T  D  K
 361 GGAGTGATCCATGGTCTGGAGAAAGTTCTGGAAATTCAGAAGAACAGATGTGACAATAATGACACCATTATTGTGAGAGGGGAGTGTGGAAAGTGTTCCCAGCAAGCCCCCTGCCCACTC
 121 G  V  I  H  G  L  E  K  V  L  E  I  Q  K  N  R  C  D  N  N  D  T  I  I  V  R  G  E  C  G  K  C  S  Q  Q  A  P  C  P  L
 481 GAGACAAAACCACTTAGAGAGACGAGGAAATGCATCTATTCCATCTACTTCATGGGAAGAGATCCGTATTCATCGGGTGCCAGCCACAGTGTGTGAGAACCATCATTACAAGAGCCTGC
 161 E  T  K  P  L  R  E  T  R  K  C  I  Y  S  I  Y  F  M  G  K  R  S  V  F  I  G  C  Q  P  Q  C  V  R  T  I  I  T  R  A  C
 601 TGGCTGGCTTCTTTGGCCCACAATGCCAAGCCTGCCCCGGGAGAGGTCAAAATGTGTGCTCTGGGAACGGCTTCTGTCTGGGACGGTGTGAATGGCACTGGCACGTGCCAGTGCGGGCTG
 201 W  L  A  S  L  A  H  N  A  K  P  A  P  G  E  V  K  M  C  A  L  G  T  A  S  V  W  D  G  V  N  G  T  G  T  C  Q  C  G  L
 721 GGCTTCAATGGGACAGCCTGTGAAACCTGCACTGAGGGGAAGTATGGTATCCACTGCGACCAAGCATGCTCTTGTGTCCATGGGAGATGTAGCCAAGGACCCTTGGGAGACGGCTCCTGT
 241 G  F  N  G  T  A  C  E  T  C  T  E  G  K  Y  G  I  H  C  D  Q  A  C  S  C  V  H  G  R  C  S  Q  G  P  L  G  D  G  S  C
 841 GACTGTGACGTCGGCTGGCGAGGAGTGAAGTGTGACATGGAGATCACCACAGACAACTGCAACGGGACCTGTCACACCAGTGCCAACTGCCTTCTGGATCCAGACGGCAAAGCCTCGTGC
 281 D  C  D  V  G  W  R  G  V  K  C  D  M  E  I  T  T  D  N  C  N  G  T  C  H  T  S  A  N  C  L  L  D  P  D  G  K  A  S  C
 961 AAATGTGCGGCAGGATTCCGAGGGAATGGAACGGTCTGCACAGCCATCAATGCCTGTGAGACCAGCAATGGAGGATGTTCTACAAAGGCCGACTGTAAAAGAACCACCCCAGGAAACCGG
 321 K  C  A  A  G  F  R  G  N  G  T  V  C  T  A  I  N  A  C  E  T  S  N  G  G  C  S  T  K  A  D  C  K  R  T  T  P  G  N  R
 081 GTGTGTGTGTGCAAGGCAGGCTATACCGGCGACGGCATCGTGTGCCTTGAAATCAACCCGTGTTTGGAGAACCATGGTGGCTGTGACAGAAATGCAGAGTGCACACAGACAGGGCCCAAC
 361 V  C  V  C  K  A  G  Y  T  G  D  G  I  V  C  L  E  I  N  P  C  L  E  N  H  G  G  C  D  R  N  A  E  C  T  Q  T  G  P  N
 201 CAGGCCGTCTGTAACTGCTTGCCGAAGTACACTGGAGATGGAAAGGTCTGCTCGCTTATCAATGTCTGCCTAACGAACAATGGCGGCTGCAGTCCATTTGCCTTCTGCAACTACACTGAG
 401 Q  A  V  C  N  C  L  P  K  Y  T  G  D  G  K  V  C  S  L  I  N  V  C  L  T  N  N  G  G  C  S  P  F  A  F  C  N  Y  T  E
 321 CAAGATCAAAGGATATGTACCTGCAAGCCAGACTACACGGGTGATGGAATCGTCTGCCGGGGCAGCATCTACGGGGAGCTTCCCAAGAACCCTTCGACGTCCCAGTACTTCTTCCAGTTG
 441 Q  D  Q  R  I  C  T  C  K  P  D  Y  T  G  D  G  I  V  C  R  G  S  I  Y  G  E  L  P  K  N  P  S  T  S  Q  Y  F  F  Q  L
 441 CAGGAGCATGCTGTCCGAGAGCTTGCTGGACCTGGCCCCTTCACCGTGTTCGCGCCTTTGTCTAGCTCCTTCAATCATGAGCCCCGGATTAAAGACTGGGATCAGCAGGGCCTCATGTCC
 481 Q  E  H  A  V  R  E  L  A  G  P  G  P  F  T  V  F  A  P  L  S  S  S  F  N  H  E  P  R  I  K  D  W  D  Q  Q  G  L  M  S
 561 CAGGTTCTTCGCTATCACGTGGTGGGCTGCCAGCAGCTGCTGTTGGACAACCTAAAAGTGACCACAAGTGCCACGACCCTCCAAGGAGAGCCAGTTTCCATCTCTGTCTCTCAGGACACT
 521 Q  V  L  R  Y  H  V  V  G  C  Q  Q  L  L  L  D  N  L  K  V  T  T  S  A  T  T  L  Q  G  E  P  V  S  I  S  V  S  Q  D  T
 681 GTGTTCATAAACAATGAGGCGAAGGTCCTGTCCAGTGACATCATCAGCACCAATGGCGTCATCCACGTTATAGACAAGTTGCTGTCTCCCAAAAACTTGCTTATCACCCCCAAAGATGCC
 561 V  F  I  N  N  E  A  K  V  L  S  S  D  I  I  S  T  N  G  V  I  H  V  I  D  K  L  L  S  P  K  N  L  L  I  T  P  K  D  A
 801 TTGGGCAGGGTTCTGCAAAATCTTACTACAGTGGCAGCAAACCACGGATATACCAAATTCAGCAAGTTGATACAGGACTCAGGCTTGCTGTCAGTCATCACTGACTCCATCCACACCCCA
 601 L  G  R  V  L  Q  N  L  T  T  V  A  A  N  H  G  Y  T  K  F  S  K  L  I  Q  D  S  G  L  L  S  V  I  T  D  S  I  H  T  P
 921 GTCACTGTCTTCTGGCCTACGGACAAAGCCCTGGAAGCCTTGCCCCCAGAGCAGCAGGACTTCCTGTTCAATCAAGACAACAAGGACAAGCTGAAGTCTTACCTGAAGTTCCACGTGATC
 641 V  T  V  F  W  P  T  D  K  A  L  E  A  L  P  P  E  Q  Q  D  F  L  F  N  Q  D  N  K  D  K  L  K  S  Y  L  K  F  H  V  I
 041 CGAGACTCCAAGGCTTTAGCTTCAGACCTCCCCAGGTCTGCTTCCTGGAAGACCCTGCAAGGCTCAGAGCTGAGTGTGAGGTGTGGAACTGGCAGTGACATCGGTGAGCTCTTTCTAAAC
 681 R  D  S  K  A  L  A  S  D  L  P  R  S  A  S  W  K  T  L  Q  G  S  E  L  S  V  R  C  G  T  G  S  D  I  G  E  L  F  L  N
 161 GAACAAATGTGCAGATTCATACACCGGGGACTCTTGTTTGACGTGGGTGTGGCCTATGGCATTGACTGCCTACTCATGAATCCTACCCTAGGTGGCCGATGTGACACTTTTACTACCTTC
 721 E  Q  M  C  R  F  I  H  R  G  L  L  F  D  V  G  V  A  Y  G  I  D  C  L  L  M  N  P  T  L  G  G  R  C  D  T  F  T  T  F
 281 GATATTCCGGGGGAGTGCGGAAGTTGCATTTTCACTCCCAAATGCCCACTGAAGAGCAAGCCAAAGGGCGTGAAGAAGAAGTGTATCTACAACCCGTTACCTTTCAGGAGGAACGTGGAA
 761 D  I  P  G  E  C  G  S  C  I  F  T  P  K  C  P  L  K  S  K  P  K  G  V  K  K  K  C  I  Y  N  P  L  P  F  R  R  N  V  E
 401 GGCTGCCAGAACCTGTGCACCGTGGTGATCCAAACCCCCAGGTGCTGCCATGGTTACTTCATGCCAGACTGTCAGGCCTGCCCTGGAGGACCAGATACACCGTGTAACAACCGGGGCATG
 801 G  C  Q  N  L  C  T  V  V  I  Q  T  P  R  C  C  H  G  Y  F  M  P  D  C  Q  A  C  P  G  G  P  D  T  P  C  N  N  R  G  M
 521 TGCCGCGATCTGTACACACCCATGGGACAGTGCCTATGCCACACCGGCTTCAACGGGACAGCCTGCGAGCTCTGCTGGCATGGGAGATTTGGGCCTGACTGTCAGCCCCGCAGCTGCTCC
 841 C  R  D  L  Y  T  P  M  G  Q  C  L  C  H  T  G  F  N  G  T  A  C  E  L  C  W  H  G  R  F  G  P  D  C  Q  P  R  S  C  S
 641 GAGCATGGACAGTGTGATGAGGGGATCACAGGCTCCGGGGAGTGCCTCTGTGAAACAGGGTGGACAGCCGCTTCGTGTGACACTCCCACAGCTGTATTCGCAGTGTGCACACCTGCTTGC
 881 E  H  G  Q  C  D  E  G  I  T  G  S  G  E  C  L  C  E  T  G  W  T  A  A  S  C  D  T  P  T  A  V  F  A  V  C  T  P  A  C
 761 TCCGTGCACGCCACCTGTACGGAGAACAACACGTGTGTGTGTAACTTGAACTACGAAGGTGACGGGATCACATGCACAGTCGTGGACTTCTGCAAACAGAACAACGGGGGCTGTGCGAAG
 921 S  V  H  A  T  C  T  E  N  N  T  C  V  C  N  L  N  Y  E  G  D  G  I  T  C  T  V  V  D  F  C  K  Q  N  N  G  G  C  A  K
 881 GTCGCTAAGTGCTCCCAGAAAGGCACCCAAGTCTCTTGCAGCTGCAAGAAAGGCTACAAGGGGGATGGCTACAGCTGCATAGAGATAGACCCCTGTGCAGACGGTGTCAACGGGGGATGC
 961 V  A  K  C  S  Q  K  G  T  Q  V  S  C  S  C  K  K  G  Y  K  G  D  G  Y  S  C  I  E  I  D  P  C  A  D  G  V  N  G  G  C
 001 CATGAGCACGCCACCTGCAGGATGACGGGCCCAGGCAAGCATAAGTGTGAATGTAAAAGTCACTATGTCGGGGACGGAGTGGACTGTGAGCCTGAGCAGCTGCCGCTCGACCGTTGCTTA
 001 H  E  H  A  T  C  R  M  T  G  P  G  K  H  K  C  E  C  K  S  H  Y  V  G  D  G  V  D  C  E  P  E  Q  L  P  L  D  R  C  L
 121 CAGGACAACGGACAGTGCCACCCAGATGCCAGCTGTGCAGACCTCTACTTCCAGGACACGACCGTAGGAGTATTCCATCTACGCTCCCCACTGGGCCAGTACAAACTGACATTTGACAAA
 041 Q  D  N  G  Q  C  H  P  D  A  S  C  A  D  L  Y  F  Q  D  T  T  V  G  V  F  H  L  R  S  P  L  G  Q  Y  K  L  T  F  D  K
 241 GCCAAAGAAGCCTGTGCCAAAGAAGCTGCGACCATAGCCACCTACAACCAGCTCTCCTATGCCCAGAAGGCCAAGTATCACCTGTGCTCGGCCGGCTGGCTGGAGAGTGGGCGGGTTGCC
 081 A  K  E  A  C  A  K  E  A  A  T  I  A  T  Y  N  Q  L  S  Y  A  Q  K  A  K  Y  H  L  C  S  A  G  W  L  E  S  G  R  V  A
 361 TACCCGACTACGTATGCCTCTCAGAAGTGTGGTGCAAACGTTGTTGGGATCGTAGACTACGGATCCAGGGCCAACAAGAGTGAAATGTGGGATGTCTTCTGTTACCGGATGAAAGATGTG
 121 Y  P  T  T  Y  A  S  Q  K  C  G  A  N  V  V  G  I  V  D  Y  G  S  R  A  N  K  S  E  M  W  D  V  F  C  Y  R  M  K  D  V
 481 AACTGCACCTGCAAGGCAGGCTATGTGGGAGATGGCTTCTCGTGCAGTGGGAACCTGCTGCAGGTCCTCATGTCCTTCCCCTCGCTCACAAACTTCCTGACAGAGGTGCTGGCTTTTTCC
 161 N  C  T  C  K  A  G  Y  V  G  D  G  F  S  C  S  G  N  L  L  Q  V  L  M  S  F  P  S  L  T  N  F  L  T  E  V  L  A  F  S
 601 AAGAGCTCAGCCCGAGGACAGGCATTTTTGAAACACCTGACTGACCTGTCCATCCGTGGCACCCTGTTTGTGCCACAGAACAGTGGGCTACCGGGAAATAAGAGCCTGTCTGGCCGGGAC
 201 K  S  S  A  R  G  Q  A  F  L  K  H  L  T  D  L  S  I  R  G  T  L  F  V  P  Q  N  S  G  L  P  G  N  K  S  L  S  G  R  D
 721 ATTGAGCACCACCTCACTAATGTCAACGTCTCCTTTTACAATGACCTTGTCAATGGTACCTTTCTGAGGACTATGCTGGGAAGCCAACTGCTCATTACCTTCAGCCAGGACCAGCTCCAC
 241 I  E  H  H  L  T  N  V  N  V  S  F  Y  N  D  L  V  N  G  T  F  L  R  T  M  L  G  S  Q  L  L  I  T  F  S  Q  D  Q  L  H
 841 CAAGAGACCAGGTTTGTGGATGGAAGATCCATTCTGCAGTGGGACATCATCGCCGCCAATGGAATCCTCCATATTATTTCTGAACCTTTGAGAGCTCCTCCCACGGCAGCAACGGCTGCC
 281 Q  E  T  R  F  V  D  G  R  S  I  L  Q  W  D  I  I  A  A  N  G  I  L  H  I  I  S  E  P  L  R  A  P  P  T  A  A  T  A  A
 961 CACTCTGGCCTGGGGACAGGTATATTCTGTGCCGTCGTCCTGGTCACTGGTGCGATTGCTCTGGCAGCTTACTCTTACTTCCGGCTAAAGCAGCGAACCACTGGTTTCCAGCGTTTTGAT
 321 H  S  G  L  G  T  G  I  F  C  A  V  V  L  V  T  G  A  I  A  L  A  A  [illegible]  K  Q  R  T  T  G  [illegible]  D
 081 CAGAAGAGGACATTGATGTCTTGGCTTTTGGCAAGCAGCAGCCCAAGAATATCGCAAACCCTCTGTATGAGACCTCAGCGCCGGCACCCCCAGAGTCCTCCTGTGACCCCTTCACAGACC
 361 Q  K  R  T  L  M  S  W  [illegible]  A  S  S  S  P  R  I  S  Q  T  L  C  M  R  P  Q  R  R  H  P  Q  S  P  P  V  T  P  S  Q  T
 201 CTGGAGAACAGGATCTGGAGGACAGCGACCCTCTGGGGGCACTGCGGTCCTGACATGAGAAGCCAGCAAGCAACCACAGTCACGGTTCCACGGTGATTCCCAGCCCCAGCTGTCTCATGG
 401 L  E  N  R  I  W  R  T  A  T  L  W  G  H  C  G  P  D  M  R  S  Q  Q  A  T  T  V  T  V  P  R  *

 321 ATCAGTTGTTTTAAAGAATGACAACACTCATAAGCCAGCCATACCTCACCCTTCTGGTTAATCTGGGATTGTCGCCAGGGCTAAGGAGCCATGTTGCCTGGATACCTGGGGGACCTCCAC
 441 CTCCTCTGAGCCTATACCGTGGTTCTCTCACTTCCATATGGTGCTTGGTCTGTTCTGCCCTCTCTTGTACCCACAAACTGTGACTCTGTGGTATTCTCCTATTGACGTAAGCACCAAAGG
 561 CGGGGCTTCACCTCTTATGTTCTGTATTCCAGTACCCAGAAGTACCTGCCACACATGTGTGCTCAATAAATGTTTTGGGAACAAAATAAAGAAGGCACTGTGTACCTAGAAGGTGTCAAA
 681 CTATGAAAGCAAAAAAAAAAAAAAAA
```

Figure 22

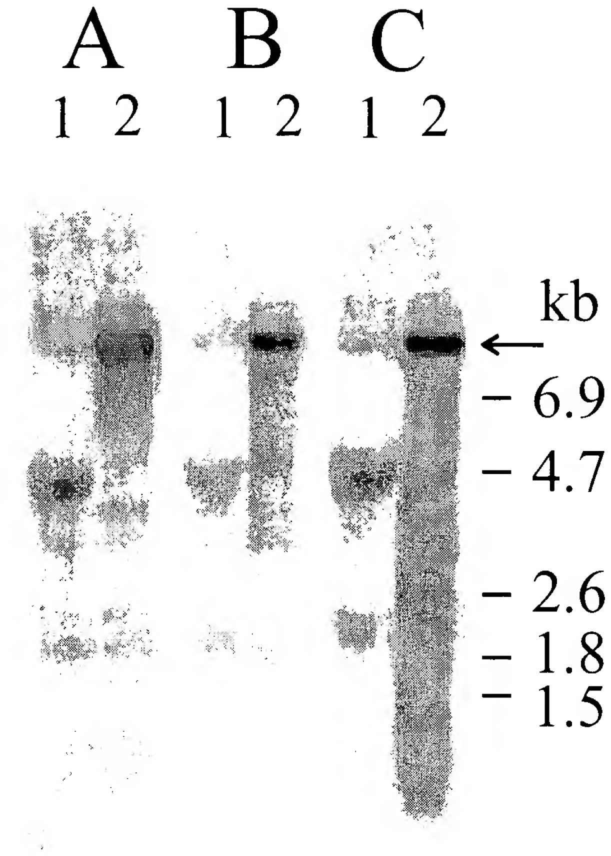

A
B
C
1
2
1
2
1
2
kb
6.9
4.7
2.6
1.8
1.5

Figure 23

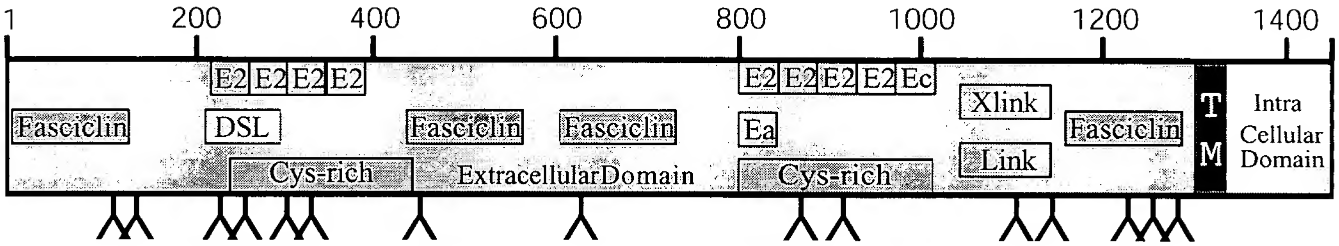

1
200
400
600
800
1000
1200
1400
E2
E2
E2
E2
Fasciclin
DSL
Cys-rich
Fasciclin
Fasciclin
ExtracellularDomain
E2
E2
E2
E2
Ec
Ea
Cys-rich
Xlink
Link
Fasciclin
T
M
Intra
Cellular
Domain

Figure 24

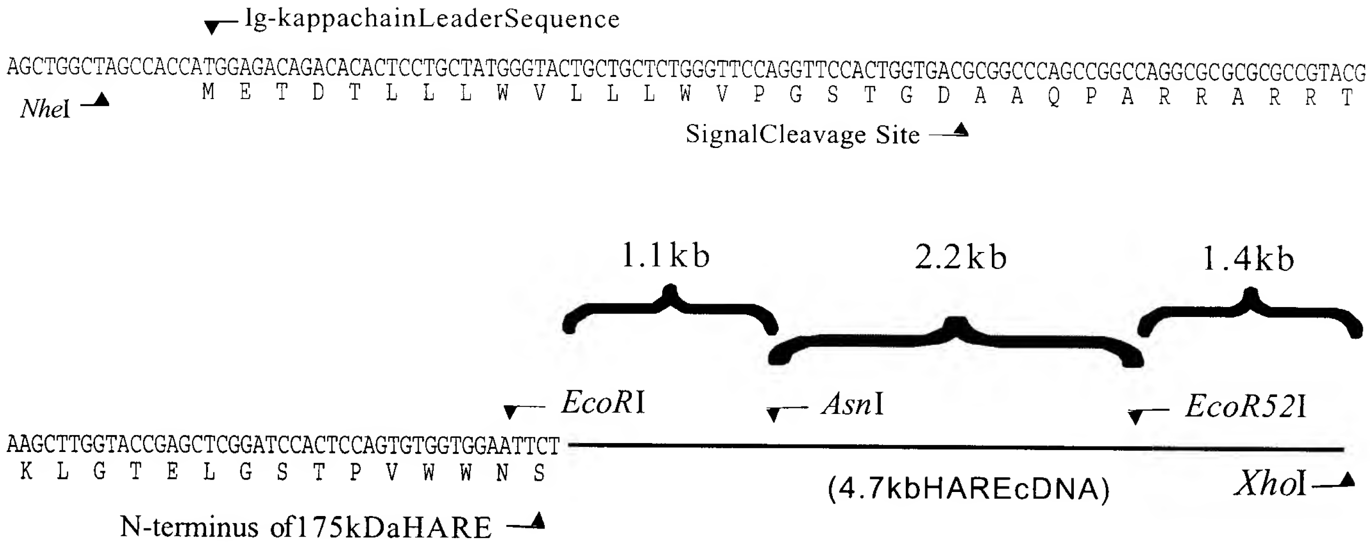
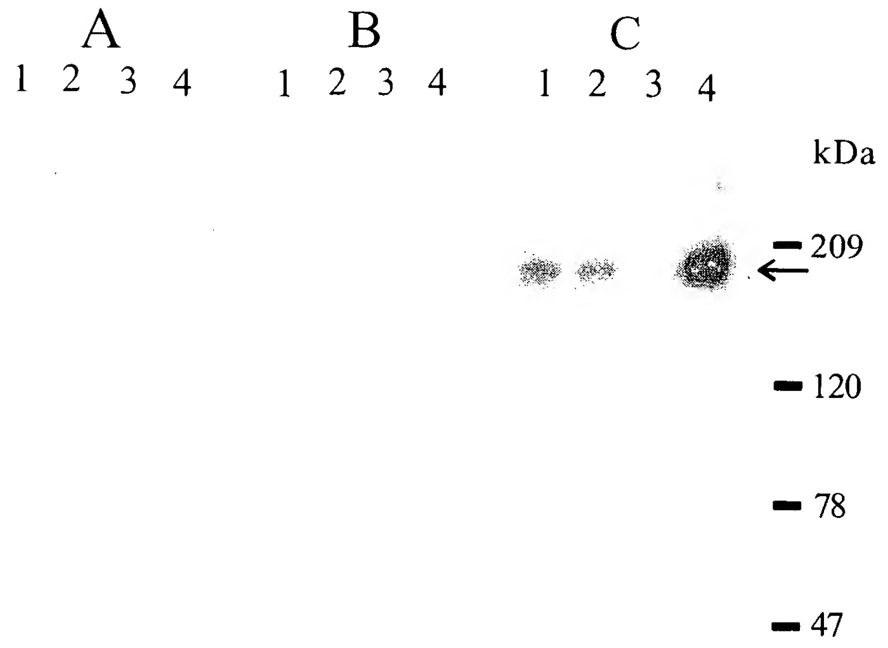

Ig-kappachainLeaderSequence
AGCTGGCTAGCCACCATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTGGGTTCCAGGTTCCACTGGTGACGCGGCCCAGCCGGCCAGGCGCGCGCGCCGTACG
NheI
M E T D T L L L W V L L L W V P G S T G D A A Q P A R R A R R T
SignalCleavage Site
1.1kb
2.2kb
1.4kb
EcoRI
AsnI
EcoR52I
AAGCTTGGTACCGAGCTCGGATCCACTCCAGTGTGGTGGAATTCT
K L G T E L G S T P V W W N S
(4.7kbHAREcDNA)
XhoI
N-terminus of175kDaHARE

Figure 25

Autoradiography


A
B
C
1 2 3 4
1 2 3 4
1 2 3 4
kDa
209
120
78
47

Western Blot

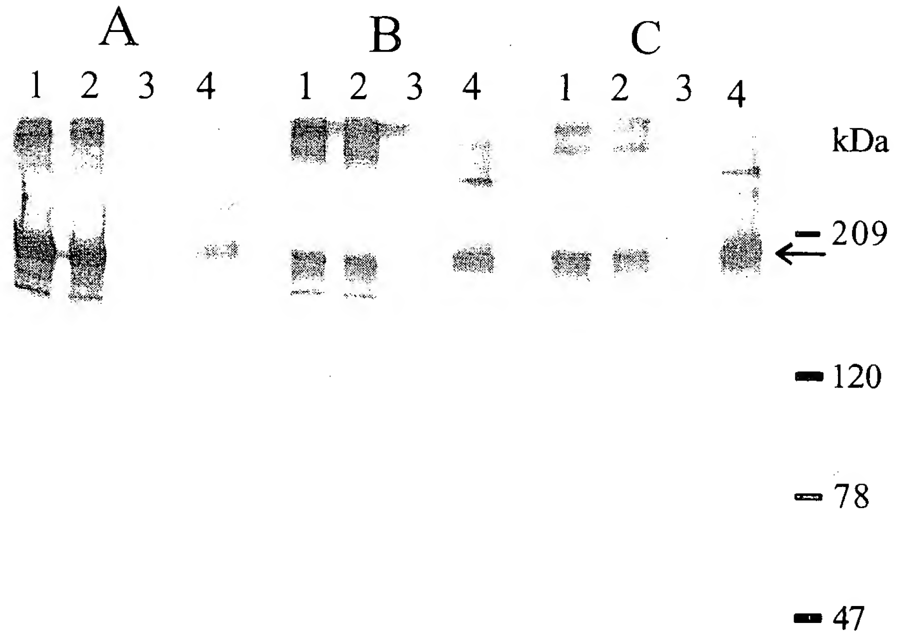

A
B
C
1 2 3 4
1 2 3 4
1 2 3 4
kDa
209
120
78
47

Figure 26

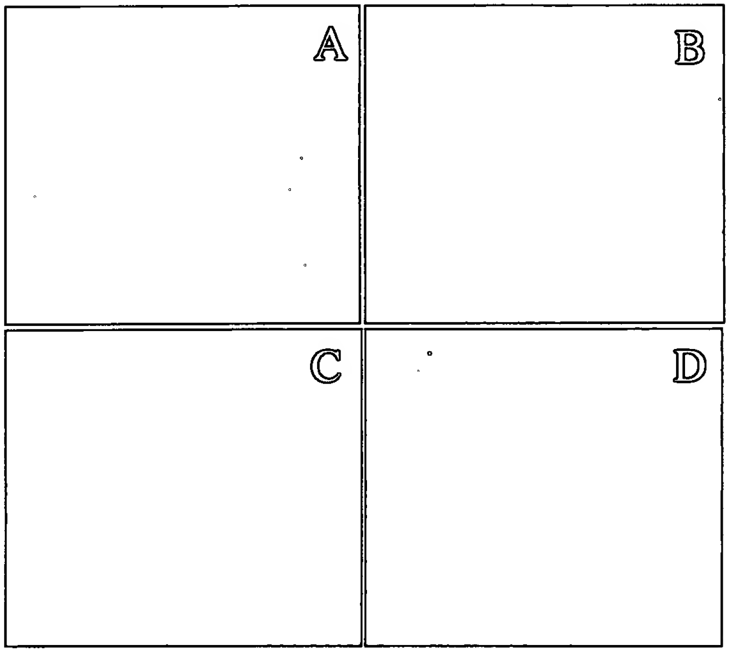
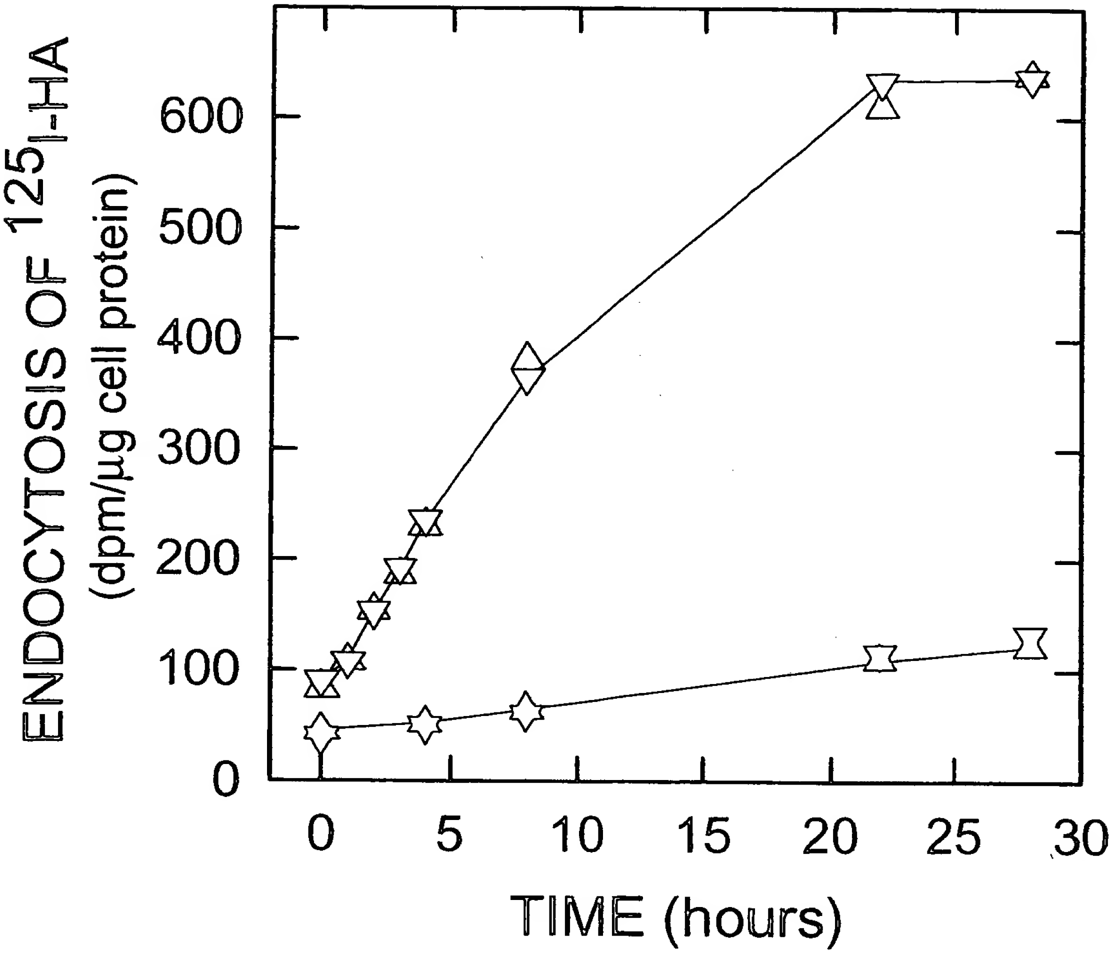


Figure 27A



ENDOCYTOSIS OF ^{125}I-HA
(dpm/µg cell protein)
0
100
200
300
400
500
600
0
5
10
15
20
25
30
TIME (hours)

Figure 27B

Degradation of internalized HA by transfected SK-Hep1 cell lines expressing the 175-kDa HARE

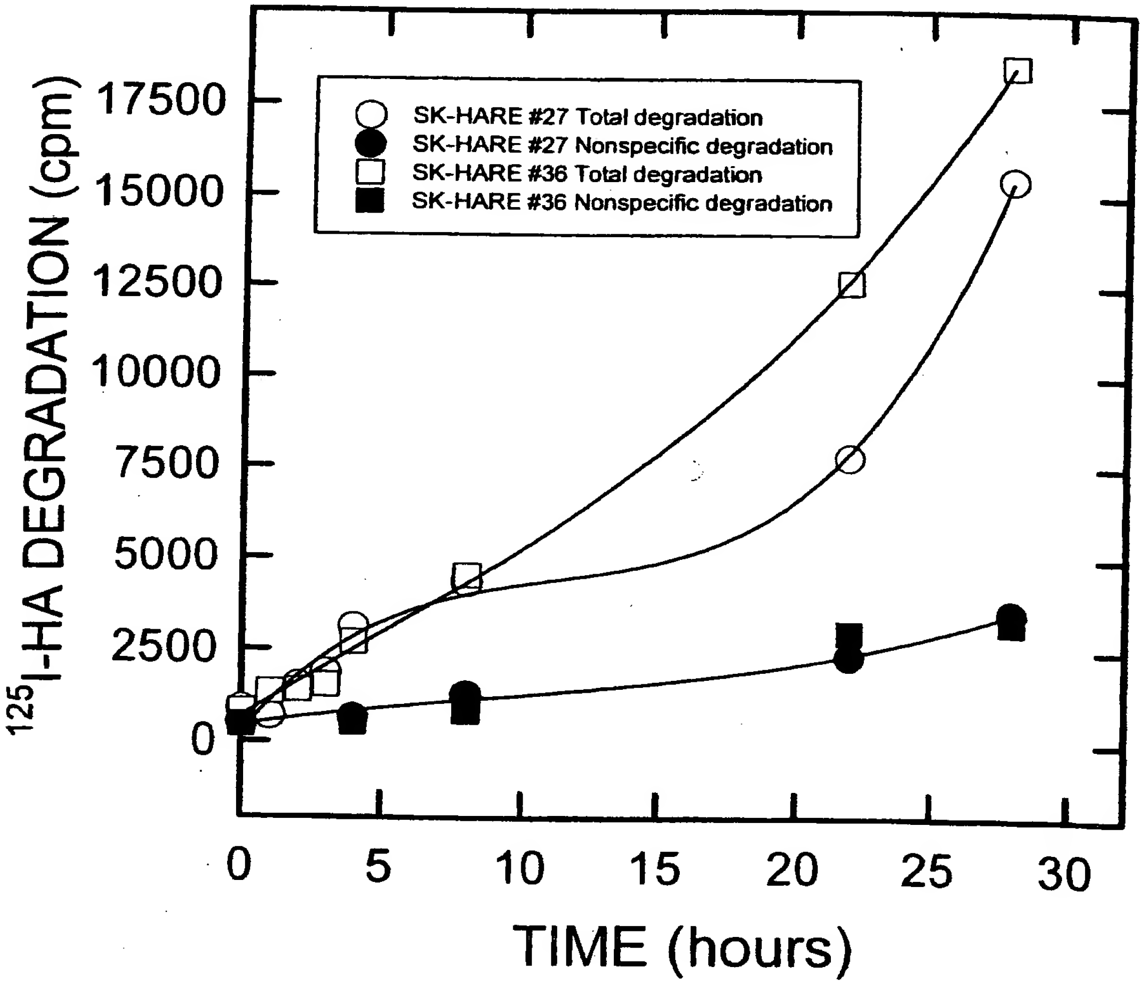


Figure 27C

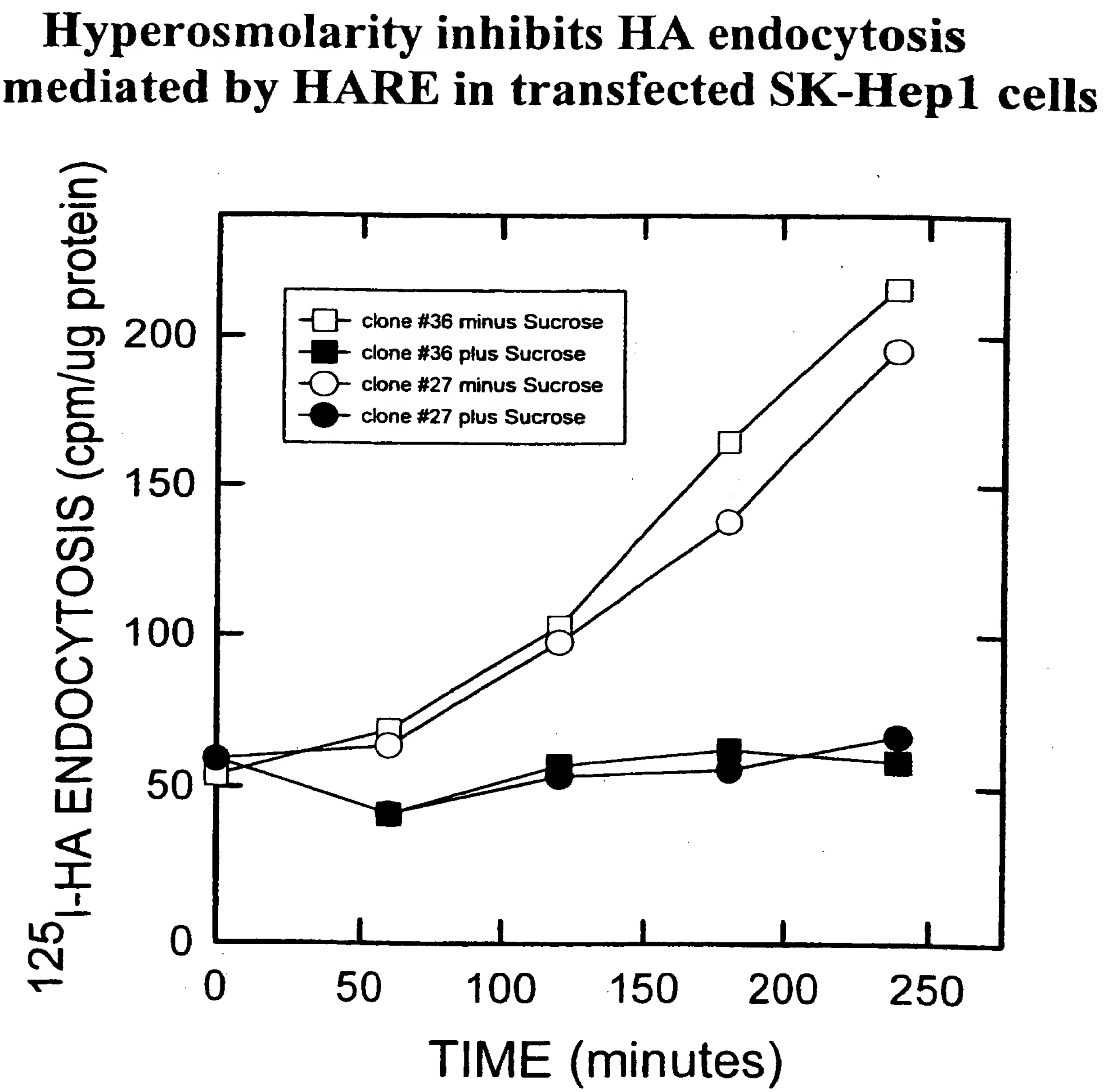

Hyperosmolarity inhibits HA endocytosis mediated by HARE in transfected SK-Hep1 cells
clone #36 minus Sucrose
clone #36 plus Sucrose
clone #27 minus Sucrose
clone #27 plus Sucrose
^{125}I-HA ENDOCYTOSIS (cpm/ug protein)
0
50
100
150
200
0
50
100
150
200
250
TIME (minutes)

Figure 27D

Specific monoclonal antibodies against HARE inhibit HA endocytosis in SK-Hep1 transfectants expressing the 175-kDa HARE

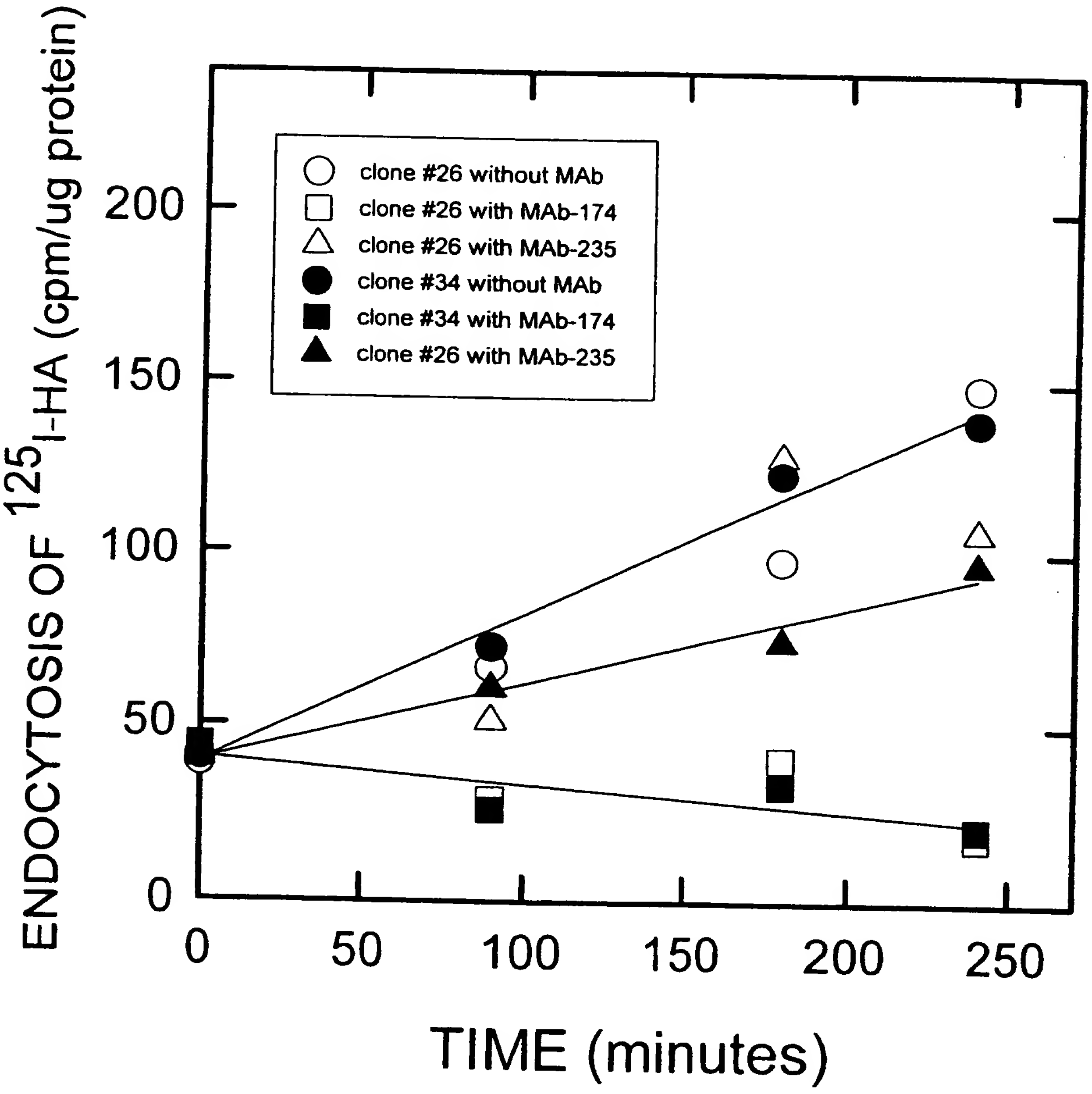


Figure 28

```
175HARE      1 ---------- ------SLPS LLTRLEQMPD YSIFRGYIIH YNLASAIESA DAYTVFVPNN EAIENYIREK KATSLKEDIL RYHVVLGEKL LKNDLHNGMH RETMLGFSYL
CAB61827  1111 LHILSQVLLP PRGDVPGGQG LLQQLDLVPA FSLFRELLQH HGLVPQIEAA TAYTIFVPTN RSLEA---QG NSSHLDADTV RHHVVLGEAL SMETLRKGGH RNSLLGPAHW
BAA13377   754 LHILSQVLLP PRGDVPGGQG LLQQLDLV-A FSLFRELLQH HGLVPQIEAA TAYTIFVPTN RSLEA---QG NSSHLDADTV RHHVVLGEAL SMETLRKGGH RNSLLGPAHW

175HARE     95 LAFFLRNDQL YVNEAPINYT NVATDKGVIH GLEKVLEIQK NRDNNDTII VRGEGKSQ QAPLETKP LRETRK-IY SIYFMGKRSV FIGQPQVR TIITRAWLA
CAB61827  1218 IVFYNHSGQP EVNHVPLEGP MLEAPGRSLI GLSGVLTVGS SRLHSHAEA LREKVNTR RFRTQGFQL QDTPRKSVY RSGFSFSR-- --GSYTAK KIQVPDCPG
BAA13377   861 IVFYNHSGQP EVNHVPLEGP MLEAPGRSLI GLSGVLTVGS SRLHSHAEA LREKVNTR RFRTQGFQL QDTPRKSVY RSGFSFSR-- --GSYTAK KIQVPDCPG

175HARE    204 SLAHNAKPAP GEVK-MALG TASVWDGVNG TGTQGLGF NGTAETTE GKYGIHDQA SVHGRSQ GPLGDGSD DVGWRGVKD MEITTDNNG THTSANLL
BAB15793     1 ---------- ---------W HLFGWS--DG TGVEGEGF SGTAETTE GKYGIHDQA SVHGRNQ GPLGDGSD DVGWRGVHD NATTEDNNG THTSANLT
CAB61358     1 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- --------VG
CAB61827  1224 FFGTLCEPCP GGLGGVS-G HGQCQDRFLG SGEHHEGF HGTAEVEL GRYGPNTGV DAHGLQE GLQGDGSM NVGWQGLRD QKITSPQPR KDPNANVQ
BAA13377   967 FFGTLCEPCP GGLGGVS-G HGQCQDRFLG SGEHHEGF HGTAEVEL GRYGPNTGV DAHGLQE GLQGDGSM NVGWQGLRD QKITSPQPR KDPNANVQ

175HARE    313 DPDGKASK AAGFRGNGTV TAINAETS NGGSTKAL KRTTPGNRV VKAGYTGDG IVLEINPL ENHGGDRNA ETQTGPNQA VNLPKYTG DG-KVSLIN
BAB15793    90 NSDGTASK AAGFQGNGTI TAINAEIS NGGSAKAD KRTTPGRRV TKAGYTGDG IVLEINPL ENHGGDKNA ETQTGPNQA ANLPAYTG DG-KVTLIN
CAB61358     3 EAVGTASK AAGFQGNGTI TAINAEIS NGGSAKAD KRTTPGRRV TKAGYTGDG IVLEINPL ENHGGDKNA ETQTGPNQA ANLPAYTG DG-KVTLIN
CAB61827  1433 DSAGASTA AAGYSGNGIF SEVDPAHG HGGSPHAN TKVAPGQRT TQDGYMGDG ELQEINSL IHHGGHIHA EIPTGPQQV SSREGYSG DGIRTELLD
BAA13377  1076 DSAGASTA AAGYSGNGIF SEVDPAHG HGGSPHAN TKVAPGQRT TQDGYMGDG ELQEINSL IHHGGHIHA EIPTGPQQV SSREGYSG DGIRTELLD

175HARE    422 VLTNNGGS PFAFNYTEQ DQRITKPD Y-TGDGIVR GSIYGELPKN PSTSQYFFQL QEHAVRELAG PGPFTVFAP- --LSSSFNHE PRIKDWDQQG LMSQVLRYHV
BAB15793   199 VLTKNGGS EFAINHTGQ VERTIKPN Y-IGDGFTR GSIYQELPKN PKTSQYFFQL QEHFVKDLVG PGPFTVFAP- --LSAAFDEE ARVKDWDKYG LMPQVLRYHV
CAB61358   112 VLTKNGGS EFAINHTGQ VERTIKPN Y-IGDGFTR GSIYQELPKN PKTSQYFFQL QEHFVKDLVG PGPFTVFAP- --LSAAFDEE ARVKDWDKYG LMPQVLRYHV
AAF82398     1 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- -MPQVLRYHV
CAB61827  1543 RSKNNGGS PYATKSTGD GQRTIDTA HTVGDGLTR ARVGLELLRD KHAS--FFSL RLLEYKELKG DGPFTIFVPH ADLMSNLSQD ELARIRAHRQ L---VFRYHV
BAA13377  1186 RSKNNGGS PYATKSTGD GQRTIDTA HTVGDGLTR ARVGLELLRD KHAS--FFSL RLLEYKELKG DGPFTIFVPH ADLMSNLSQD ELARIRAHRQ L---VFRYHV

175HARE    528 VGQQLLLDN LKVTTSATTL QGEPVSISVS QDTVFINNEA KVLSSDIIST NGVIHVIDKL LSPKNLLITP KDALGRVLQN LTTVAANHGY TKFSKLIQDS GLLSVITDSI
BAB15793   305 VAHQLLLEN LKLISNATSL QGEPIVISVS QSTVYINNKA KIISSDIIST NGIVHIIDKL LSPKNLLITP KDNSGRILQN LTTLATNNGY IKFSNLIQDS GLLSVITDPI
CAB61358   218 VAHQLLLEN LKLISNATSL QGEPIVISVS QSTVYINNKA KIISSDIIST NGIVHIIDKL LSPKNLLITP KDNSGRILQN LTTLATNNGY IKFSNLIQDS GLLSVITDPI
AAF82398    10 VAHQLLLEN LKLISNATSL QGEPIVISVS QSTVYINNKA KIISSDIIST NGIVHIIDKL LSPKNLLITP KDNSGRILQN LTTLATNNGY IKFSNLIQDS GLLSVITDPI
CAB61827  1648 VGRRLRSED LLEQGYATAL SGHPLRFSER EGSIYLNDFA RVVSSDHEAV NGILHFIDRV LLPPEALHWE PDDAPIPRRN VTAAAQGFGY KIFSGLLKVA GLLPLLREAS
BAA13377  1291 VGRRLRSED LLEQGYATAL SGHPLRFSER EGSIYLNDFA RVVSSDHEAV NGILHFIDRV LLPPEALHWE PDDAPIPRRN VTAAAQGFGY KIFSGLLKVA GLLPLLREAS

175HARE    638 HTPVTVFWPT DKALEALPPE QQDFLFNQDN KDKLKSYLKF HVIRDSKALA SDLPRSASWK TLQGSELSVR GTGSDIGEL FLNEQMRFI HRGLLFDVGV AYGIDLLMN
BAB15793   415 HTPVTLFWPT DQALHALPAE QQDFLFNQDN KDKLKEYLKF HVIRDAKVLA VDLPTSTAWK TLQGSELSVK GAGRDIGDL FLNGQTRIV QRELLFDLGV AYGIDLLID
CAB61358   328 HTPVTLFWPT DQALHALPAE QQDFLFNQDN KDKLKEYLKF HVIRDAKVLA VDLPTSTAWK TLQGSELSVK GAGRDIGDL FLNGQTRIV QRELLFDLGV AYGIDLLID
AAF82398   120 HTPVTLFWPT DQALHALPAE QQDFLFNQDN KDKLKEYLKF HVIRDAKVLA VDLPTSTAWK TLQGSELSVK GAGRDIGDL FLNGQTRIV QRELLFDLGV AYGIDLLID
CAB61827  1758 HRPFTMLWPT DAAFRALPPD RQAWLYHEDH RDKLAAILRG HMIRNVEALA SDLPNLGPLR TMHGTPISFS SRTRP-GEL MVGEDDARIV QRHLPFEGGL AYGIDQLLEP
BAA13377  1401 HRPFTMLWPT DAAFRALPPD RQAWLYHEDH RDKLAAILRG HMIRNVEALA SDLPNLGPLR TMHGTPISFS SRTRP-GEL MVGEDDARIV QRHLPFEGGL AYGIDQLLEP

175HARE    748 PTLGGRDTF TTFDIP-GE GSIFTPKP LKSKPKGVKK K--IY---- -----NPLPF R--------- ---RNVE-G QNLTVVIQT PRHGYFMP DQAPGGPD
BAB15793   525 PTLGGRDTF TTFDAS-GE GSVNTPSP RWSKPKGVKQ K--LY---- -----N-LPF K--------- ---RNLE-G RERSLVIQI PRKGYFGR DQAPGGPD
CAB61358   438 PTLGGRDTF TTFDAS-GE GSVNTPSP RWSKPKGVKQ K--LY---- -----N-LPF K--------- ---RNLE-G RERSLVIQI PRKGYFGR DQAPGGPD
AAF82398   230 PTLGGRDTF TTFDAS-GE GSVNTPSP RWSKPKGVKQ K--LY---- -----N-LPF K--------- ---RNLE-G RERSLVIQI PRKGYFGR DQAPGGPD
CAB61827  1867 PGLGARDHF ETRPLRLNT SIGLEPP EGSQEQGSPE AWRFYPKFW TSPPLHSLGL RSVWVHPSLW GRPQGLRG HRNVTTTWK PSPGHYGS EQAPGGPS
BAA13377  1510 PGLGARDHF ETRPLRLNT SIGLEPP EGSQEQGSPE AWRFYPKFW TSPPLHSLGL RSVWVHPSLW GRPQGLRG HRNVTTTWK PSPGHYGS EQAPGGPS

175HARE    833 TPNNRGMR DLYTPMGQL HTGFNGTA ELWHGRFGP DQPRSSEH GQDEGITGS GELETGWT AASDTPTAV FAVTPASV HATTENNT VNLNYEGDG
BAB15793   609 APNNRGVL DQYSATGEK NTGFNGTA EMWPGRFGP DLPCGSDH GQDDGITGS GQLETGWT GPSDTQAVL PAVTPPSA HATKENNT ENLDYEGDG
CAB61358   522 APNNRGVL DQYSATGEK NTGFNGTA EMWPGRFGP DLPCGSDH GQDDGITGS GQLETGWT GPSDTQAVL PAVTPPSA HATKENNT ENLDYEGDG
AAF82398   314 APNNRGVL DQYSATGEK NTGFNGTA EMWPGRFGP DLPCGSDH GQDDGITGS GQLETGWT GPSDTQAVL PAVTPPSA HATKENNT ENLDYEGDG
CAB61827  1977 SPSDRGVM DGMSGSGQL RSGFAGTA ELAPGAFGP HQACRTVH GRDEGLGGS GSFDEGWT GPREVQLEL QPVTPPAP EAVRAGNS ESLGYEGDG
BAA13377  1620 SPSDRGVM DGMSGSGQL RSGFAGTA ELAPGAFGP HQACRTVH GRDEGLGGS GSFDEGWT GPREVQLEL QPVTPPAP EAVRAGNS ESLGYEGDG

175HARE    943 ITTVVDRK QNNGGAKVA KSQKGTQVS SKKGYKGD GYSIEIDP ADGVNGGHE HATRMTGPG KHKEKSHY VGDGVD-EP EQLPLDRLQ DNGQHPDAS
BAB15793   719 ITTVVDRK QDNGGAKVA RSQKGTKVS SQKGYKGD GHSTEIDP ADGLNGGHE HATKMTGPG KHKEKSHY VGDGLN-EP EQLPIDRLQ DNGQHADAK
CAB61358   632 ITTVVDRK QDNGGAKVA RSQKGTKVS SQKGYKGD GHSTEIDP ADGLNGGHE HATKMTGPG KHKEKSHY VGDGLN-EP EQLPIDRLQ DNGQHADAK
AAF82398   424 ITTVVDRK QDNGGAKVA RSQKGTKVS SQKGYKGD GHSTEIDP ADGLNGGHE HATKMTGPG KHKEKSHY VGDGLN-EP EQLPIDRLQ DNGQHADAK
CAB61827  2087 RVTVADLQ DGHGGSEHA NSQVGTMVT TLPDYEGD GWSRARNP TDGHRGGSE HANLSTGLN TRREHAGY VGDGLQLEE SEPPVDRLG QPPRHSDAM
BAA13377  1730 RVTVADLQ DGHGGSEHA NSQVGTMVT TLPDYEGD GWSRARNP TDGHRGGSE HANLSTGLN TRREHAGY VGDGLQLEE SEPPVDRLG QPPRHSDAM

175HARE   1052 ADLYFQDTT VGVFHLRSPL GQYKLTFDKA KEAAKEAAT IATYNQLSYA QKAKYHLSA GWLESGRVAY PTTYASQKG ANVVGIVDYG SRANKSEMWD VFYRMKDVN
BAB15793   828 VDLHFQDTT VGVFHLRSPL GQYKLTFDKA REAANEAAT MATYNQLSYA QKAKYHLSA GWLETGRVAY PTAFASQNG SGVVGIVDYG PRPNKSEMWD VFYRMKDVN
CAB61358   741 VDLHFQDTT VGVFHLRSPL GQYKLTFDKA REAANEAAT MATYNQLSYA QKAKYHLSA GWLETGRVAY PTAFASQNG SGVVGIVDYG PRPNKSEMWD VFYRMKDVN
AAF82398   533 VDLHFQDTT VGVFHLRSPL GQYKLTFDKA REAANEAAT MATYNQLSYA QKAKYHLSA GWLETGRVAY PTAFASQNG SGVVGIVDYG PRPNKSEMWD VFYRMKG--
CAB61827  2197 TDQHFQEKR AGVFHLQATS GPYGLNFSEA EAAEAQGAV LASFPQLSAA QQLGFHLLM GWLANGSTAH PVVFPVADG NGRVGVVSLG ARKNLSERWD AYFRVQDVA
BAA13377  1840 TDLHFQEKR AGVFHLQATS GPYGLNFSEA EAAEAQGAV LASFPQLSAA QQLGFHLLM GWLANGSTAH PVVFPVADG NGRVGIVSLG ARKNLSERWD AYFRVQDVA

175HARE   1162 TKAGYVGD GFS-SGNLL QVLMSFPSLT NFLTEVLAFS KSSARGQAFL KHLTDLSIRG TLFVPQNSGL PGNKSLSGRD IEHHLTNVNV SFYNDLVNGT FLRTMLGSQL
BAB15793   938 TKVGYVGD GFS-SGNLL QVLMSFPSLT NFLTEVLAYS NSSARGRAFL EHLTDLSIRG TLFVPQNSGL GENETLSGRD IEHHLANVSM FFYNDLVNGT TLQTRLGSKL
CAB61358   849 ---------- -----SAGLF QQLSSRPCIS R--------- ---------- -TPDDLSIRG TLFVPQNSGL GENETLSGRD IEHHLANVSM FFYNDLVNGT TLQTRLGSKL
AAF82398   643 TKVGYVGD GFS-SGNLL QVLMSFPSLT NFLTEVLAYS NSSARGRAFL EHLTDLSIRG TLFVPQNSGL GENETLSGRD IEHHLANVSM FFYNDLVNGT TLQTRVGSKL
CAB61827  2307 RRNGFVGD GISTNGKLL DVLAATANFS TFYGMLLGYA NATQRGLDFL DFLDDELTYK TLFVPVNEGF VDNMTLSGPD LELHASNATL LSAN-ASQGK LLPAHSGLSL
BAA13377  1950 RRNGFVGD GISTNGKLL DVLAATANFS TFYGMLLGYA NATQRGLDFL DFLDDELTYK TLFVPVNEGF VDNMTLSGPD LELHASNATL LSAN-ASQGK LLPAHSGLSL

175HARE   1271 LITFS---QD QLHQ-ETRFV DGRSILQWDI IAANGILHII SEPLRAPPTA ATA---AHSG LGTGIFCAVV LVTGAIA--L AAYSYFRLKQ RTTG--FQRF DQKRTLMSWL
BAB15793  1047 LITAS---QD PLQPTETRFV DGRAILQWDI FASNGIIHVI SRPLKAPPAP VTL---THTG LGAGIFFAII LVTGAVA--L AAYSYFRINR RTIG--FQHF ESEEDINVAA
CAB61358   924 LITAS---QD PLQPTETRFV DGRAILQWDI FASNGIIHVI SRPLKAPPAP VTL---THTG LGAGIFFAII LVTGAVA--L AAYSYFRINR RTIG--FQHF ESEEDINVAA
AAF82398   752 LITAS---QD PLQPTETRFV DGRAILQWDI FASNGIIHVI SRPLKAPPAP VTL---THTG LGAGIFFAII LVTGAVA--L AAYSYFRINR RTIG--FQHF ESEEDINVAA
CAB61827  2416 IISDAGPDNS SWAPVAPGTV VVSRIIVWDI MAFNGIIHAL ASPLLAPPQP QAVLAPEAPP VAAGV--GAV LAAGALLGLV AGALYLRARG KPTGFGFSAF QAEDDADDDF
BAA13377  2059 IISDAGPDNS SWAPVAPGTV VVSRIIVWDI MAFNGIIHAL ASPLLAPPQP -AVLAPEAPP VAAGV--GAV LAAGALLGLV AGALYLRARG KPMGFGFSAF QAEDDADDDF

175HARE   1370 LASSSP-RIS QTLCMRPQRR HPQSPPVTPS QTLENRIWRT ATLWGHCGPD MRSQQATTVT VPR
BAB15793  1147 LGKQQPENIS NPLY-ESTTS APPEPSYDPF TDSEER---- ---------- ---QLEGNDP LRTL
CAB61358  1024 LGKQQPENIS NPLY-ESTTS APPEPSYDPF TDSEER---- ---------- ---QLEGNDP LRTL
AAF82398   852 LGKQQPENIS NPLY-ESTTS APPEPSYDPF TDSEER---- ---------- ---QLEGNDP LRTL
CAB61827  2524 SPWQ-EGTN- PTLVSVPNPV FGSDTFCEPF DD-------- -SLLEEDFPD TQRILTVK-- ----
BAA13377  2166 SPWQ-EGTN- PTLVSVPNPV FGSDTFCEPF DD-------- -SLLEEDFPD TQRILTVK-- ----
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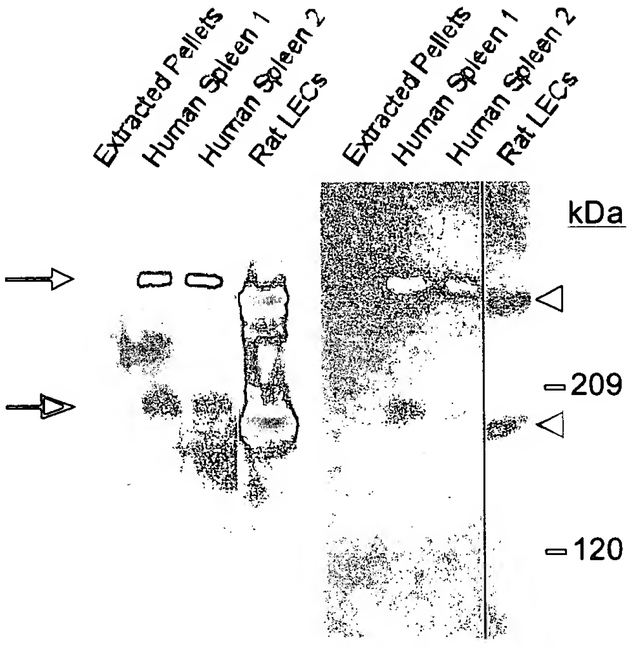
Extracted Pellets
Human Spleen 1
Human Spleen 2
Rat LECs
Extracted Pellets
Human Spleen 1
Human Spleen 2
Rat LECs
kDa
209
120

Western Blot Ligand blot

Figure 3 0

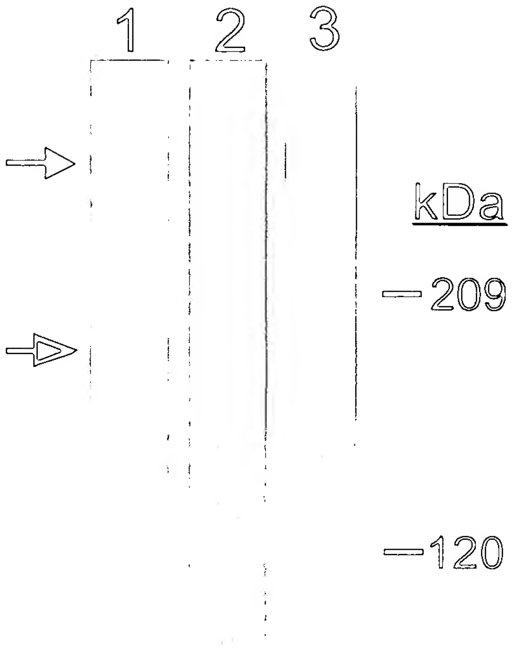
1
2
3
kDa
209
120

Figure 31

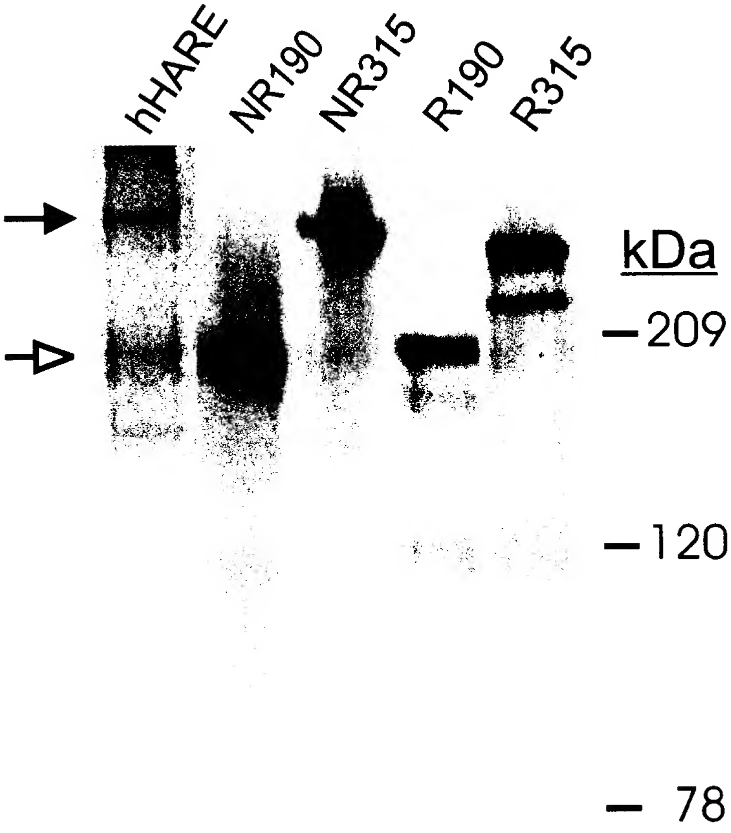
hHARE
NR190
NR315
R190
R315
kDa
209
120
78

Figure 3 2

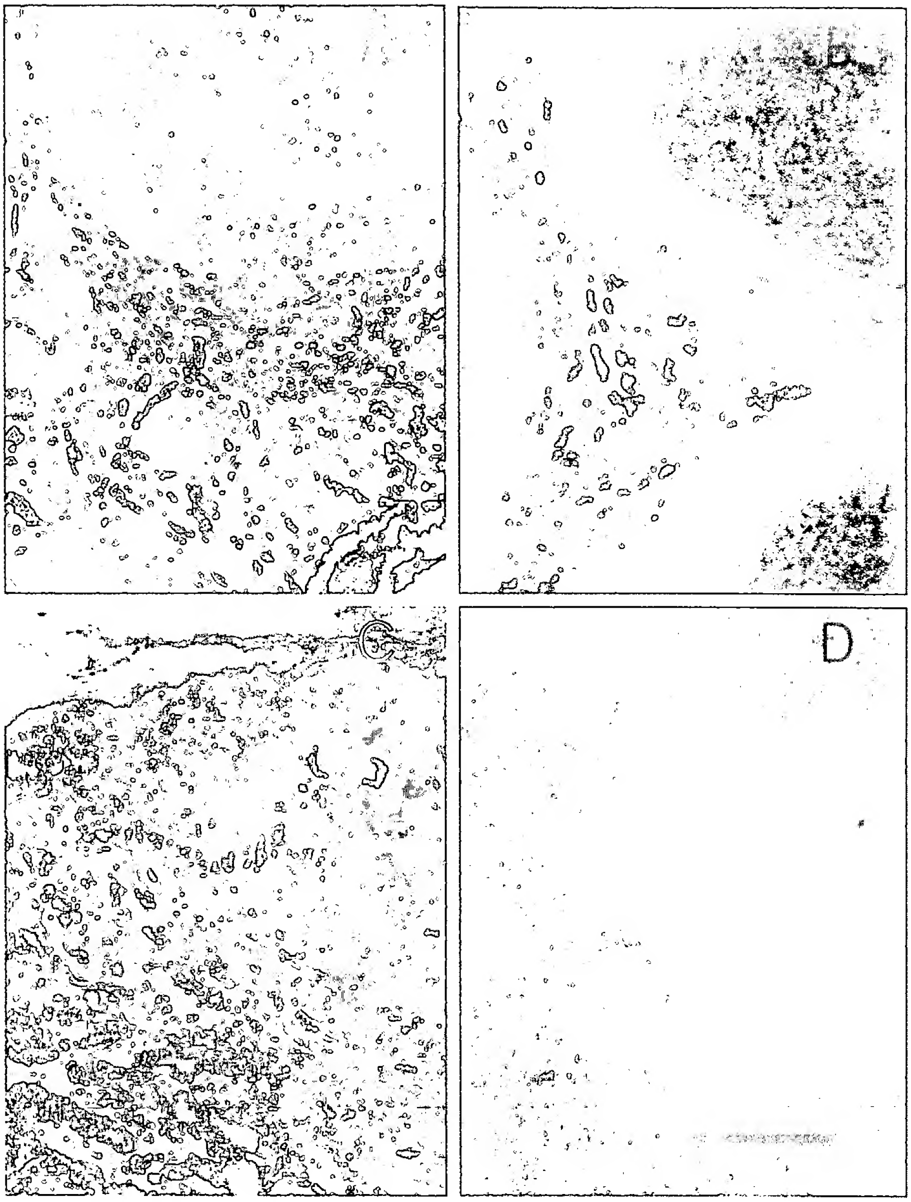

Figure 33

```
   1 ATTCAATATAATCTGGCGAATGCAATTGAGGCTGCCGATGCCTACACAGTGTTTGCTCCAAACAACAATGCCATCGAGAATTACATCAGGGAGAAGAAAGTCTTGTCTCTAGAGGAGGAC
   1 I  Q  Y  N  L  A  N  A  I  E  A  A  D  A  Y  T  V  F  A  P  N  N  N  A  I  E  N  Y  I  R  E  K  K  V  L  S  L  E  E  D
 121 GTCCTCCGGTATCATGTGGTCCTGGAGGAGAAACTCCTGAAGAATGACCTGCACAATGGCATGCATCGTGAGACCATGCTGGGTTTCTCCTATTTCCTTAGCTTCTTTCTCCATAATGAC
  41 V  L  R  Y  H  V  V  L  E  E  K  L  L  K  N  D  L  H  N  G  M  H  R  E  T  M  L  G  F  S  Y  F  L  S  F  F  L  H  N  D
 241 CAGCTCTATGTAAATGAGGCTCCAATAAACTACACCAATGTAGCCACTGATAAGGGAGTGATCCATGGCTTGGGAAAAGTTCTGGAAATTCAGAAGAACAGATGTGATAATAATGACACT
  81 Q  L  Y  V  N  E  A  P  I  N  Y  T  N  V  A  T  D  K  G  V  I  H  G  L  G  K  V  L  E  I  Q  K  N  R  C  D  N  N  D  T
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 121 T  I  I  R  G  R  C  R  T  C  S  S  E  L  T  C  P  F  G  T  K  S  L  G  N  E  K  R  R  C  I  Y  T  S  Y  F  M  G  R  R
 481 ACCCTGTTTATTGGGTGCCAGCCAAAATGTGTGAGAACCGTCATTACGAGAGAATGCTGTGCCGGCTTCTTTGGCCCCCAATGCCAGCCCTGTCCAGGGAATGCCCAGAATGTCTGCTTT
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 201 G  N  G  I  C  L  D  G  V  N  G  T  G  V  C  E  C  G  E  G  F  S  G  T  A  C  E  T  C  T  E  G  K  Y  G  I  H  C  D  Q
 721 GCATGTTCTTGTGTCCATGGGAGATGCAACCAAGGACCCTTGGGAGATGGCTCCTGTGACTGTGATGTTGGCTGGCGAGGAGTGCATTGTGACAATGCAACCACAGAAGACAACTGCAAT
 241 A  C  S  C  V  H  G  R  C  N  Q  G  P  L  G  D  G  S  C  D  C  D  V  G  W  R  G  V  H  C  D  N  A  T  T  E  D  N  C  N
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 281 G  T  C  H  T  S  A  N  C  L  T  N  S  D  G  T  A  S  C  K  C  A  A  G  F  Q  G  N  G  T  I  C  T  A  I  N  A  C  E  I
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 321 S  N  G  G  C  S  A  K  A  D  C  K  R  T  T  P  G  R  R  V  C  T  C  K  A  G  Y  T  G  D  G  I  V  C  L  E  I  N  P  C
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 361 L  E  N  H  G  G  C  D  K  N  A  E  C  T  Q  T  G  P  N  Q  A  A  C  N  C  L  P  A  Y  T  G  D  G  K  V  C  T  L  I  N
1201 GTCTGCTTAACTAAAAATGGCGGCTGTAGTGAATTTGCCATCTGCAACCACACTGGGCAAGTAGAAAGGACTTGTACTTGCAAGCCAAACTACATTGGAGATGGATTTACCTGCCGGGGC
 401 V  C  L  T  K  N  G  G  C  S  E  F  A  I  C  N  H  T  G  Q  V  E  R  T  C  T  C  K  P  N  Y  I  G  D  G  F  T  C  R  G
1321 AGCATTTATCAGGAGCTTCCCAAGAACCCGAAAACTTCCCAGTATTTCTTCCAGTTGCAGGAGCATTTCGTGAAAGATCTGGTCGGCCCAGGCCCCTTCACTGTTTTTGCACCTTTATCT
 441 S  I  Y  Q  E  L  P  K  N  P  K  T  S  Q  Y  F  F  Q  L  Q  E  H  F  V  K  D  L  V  G  P  G  P  F  T  V  F  A  P  L  S
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 521 S  N  A  T  S  L  Q  G  E  P  I  V  I  S  V  S  Q  S  T  V  Y  I  N  N  K  A  K  I  I  S  S  D  I  I  S  T  N  G  I  V
1681 CATATCATAGACAAATTGCTATCTCCCAAAAATTTGCTTATCACTCCCAAAGACAACTCTGGAAGAATTCTGCAAAATCTTACGACTTTGGCAACAAACAATGGCTACATCAAATTTAGC
 561 H  I  I  D  K  L  L  S  P  K  N  L  L  I  T  P  K  D  N  S  G  R  I  L  Q  N  L  T  T  L  A  T  N  N  G  Y  I  K  F  S
1801 AACTTAATACAGGACTCAGGTTTGCTGAGTGTCATCACCGATCCCATCCACACCCCAGTCACTCTCTTCTGGCCCACCGACCAAGCCCTCCATGCCCTACCTGCTGAACAACAGGACTTC
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 641 L  F  N  Q  D  N  K  D  K  L  K  E  Y  L  K  F  H  V  I  R  D  A  K  V  L  A  V  D  L  P  T  S  T  A  W  K  T  L  Q  G
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 681 S  E  L  S  V  K  C  G  A  G  R  D  I  G  D  L  F  L  N  G  Q  T  C  R  I  V  Q  R  E  L  L  F  D  L  G  V  A  Y  G  I
2161 GACTGTCTGCTGATTGATCCCACCCTGGGGGGCCGCTGTGACACCTTTACTACTTTCGATGCCTCGGGGGAGTGTGGGAGCTGTGTCAATACTCCCAGCTGCCCAAGGTGGAGTAAACCA
 721 D  C  L  L  I  D  P  T  L  G  G  R  C  D  T  F  T  T  F  D  A  S  G  E  C  G  S  C  V  N  T  P  S  C  P  R  W  S  K  P
2281 AAGGGTGTGAAGCAGAAGTGTCTCTACAACCTGCCCTTCAAGAGGAACCTGGAAGGCTGCCGGGAGCGGTGCAGCCTGGTGATACAGATCCCCAGGTGCTGCAAGGGCTACTTCGGGCGA
 761 K  G  V  K  Q  K  C  L  Y  N  L  P  F  K  R  N  L  E  G  C  R  E  R  C  S  L  V  I  Q  I  P  R  C  C  K  G  Y  F  G  R
2401 GACTGTCAGGCCTGCCCTGGAGGACCAGATGCCCCGTGTAATAACCGGGGTGTCTGCCTTGATCAGTACTCGGCCACCGGAGAGTGTAAATGCAACACCGGCTTCAATGGGACGGCGTGT
 801 D  C  Q  A  C  P  G  G  P  D  A  P  C  N  N  R  G  V  C  L  D  Q  Y  S  A  T  G  E  C  K  C  N  T  G  F  N  G  T  A  C
2521 GAGATGTGCTGGCCGGGGAGATTTGGGCCTGATTGTCTGCCCTGTGGCTGCTCAGACCACGGACAGTGCGATGATGGCATCACGGGCTCCGGGCAGTGCCTCTGTGAAACGGGGTGGACA
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3361 AGACCCAACAAGAGTGAAATGTGGGATGTCTTCTGCTATCGGATGAAAGATGTGAACTGCACCTGCAAGGTGGGCTATGTGGGAGATGGCTTCTCATGCAGTGGGAACCTGCTGCAGGTC
1121 R  P  N  K  S  E  M  W  D  V  F  C  Y  R  M  K  D  V  N  C  T  C  K  V  G  Y  V  G  D  G  F  S  C  S  G  N  L  L  Q  V
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1281 I  I  H  V  I  S  R  P  L  K  A  P  P  A  P  V  T  L  T  H  T  G  L  G  A  G  I  F  F  A  I  I  L  V  T  G  A  V  A  L
3961 GCTGCTTACTCCTACTTTCGGATAAACCGGAGAACAATCGGCTTCCAGCATTTTGAGTCGGAAGAGGACATTAATGTTGCAGCTCTTGGCAAGCAGCAGCCTGAGAATATCTCGAACCCC
1321 A  A  Y  S  Y  F  R  I  N  R  R  T  I  G  F  Q  H  F  E  S  E  E  D  I  N  V  A  A  L  G  K  Q  Q  P  E  N  I  S  N  P
4081 TTGTATGAGAGCACAACCTCAGCTCCCCCAGAACCTTCCTACGACCCCTTCACGGACTCTGAAGAACGGCAGCTTGAGGGCAATGACCCCTTGAGGACACTGTGAGGGCCTGGACGGGAG
1361 L  Y  E  S  T  T  S  A  P  P  E  P  S  Y  D  P  F  T  D  S  E  E  R  Q  L  E  G  N  D  P  L  R  T  L  • (1394aa)

4201 ATGCCAGCCATCACTCACTGCCACCTGGGCCATCAACTGTGAATTCTCAGCACCAGTTGCCTTTTAGGAACGTAAAGTCCTTTAAGCACTCAGAAGCCATACCTCATCTCTCTGGCTGAT
4321 CTGGGGGTTGTTTCTGTGGGTGAGAGATGTGTTGCTGTGCCCACCCAGTACAGCTTCCTCCTCTGACCCTTTGGCTCTTCTTCCTTTGTACTCTTCAGCTGGCACCTGCTCCATTCTGCC
4441 CTACATGATGGGTAACTGTGATCTTTCTTCCCTGTTAGATTGTAAGCCTCCGTCTTTGTATCCCAGCCCCTAGCCCAGTGCCTGACACAGGAACTGTGCACAATAAAGGTTTATGGAACA
4561 GAAACAAAGTCAACAG
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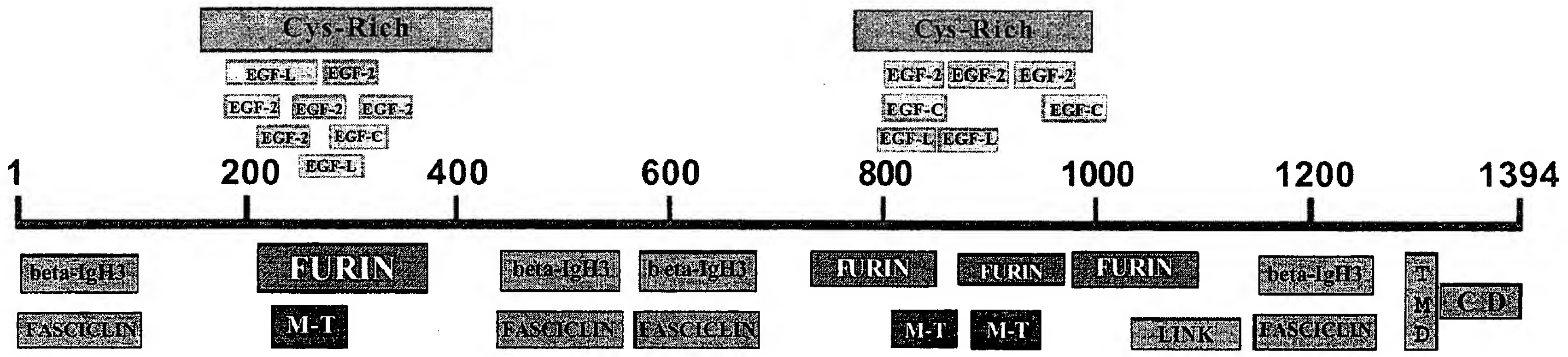
Figure 34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EGF-L
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EGF-2
EGF-2
EGF-C
EGF-C
EGF-L
EGF-L
1
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400
600
800
1000
1200
1394
beta-IgH3
FASCICLIN
FURIN
M-T
beta-IgH3
FASCICLIN
beta-IgH3
FASCICLIN
FURIN
FURIN
M-T
M-T
FURIN
LINK
beta-IgH3
FASCICLIN
T
M
D
C D

Figure 35

```
hHARE    1 IQYNLANAIEAADAYTVFAP NNNAIENYIREKKVLSLEED VLRYHVVLEEKLLKNDLHNG MHRETMLGFSYFLSFFLHND QLYVNEAPINYTNVATDKGV
rHARE   23 IHYNLASAIESADAYTVFVP NNEAIENYIREKKATSLKED ILRYHVVLGEKLLKNDLHNG MHRETMLGFSYLLAFFLRND QLYVNEAPINYTNVATDKGV

hHARE  101 IHGLGKVLEIQKNRCDNNDT TIIRGRCRTCSSELTCPFGT KSLGNEKRRCIYTSYFMGRR TLFIGCQPKCVRTVITRECC AGFFGPQCQPCPGNAQNVCF
rHARE  123 IHGLEKVLEIQKNRCDNNDT IIVRGECGKCSQQAPCPLET KPL-RETRKCIYSIYFMGKR SVFIGCQPQCVRTIITRACW LASLAHNAKPAPGEVKMCAL

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rHARE  222 GTASVWDGVNGTGTCQCGLG FNGTACETCTEGKYGIHCDQ ACSCVHGRCSQGPLGDGSCD CDVGWRGVKCDMEITTDNCN GTCHTSANCLLDPDGKASCK

hHARE  301 CAAGFQGNGTICTAINACEI SNGGCSAKADCKRTTPGRRV CTCKAGYTGDGIVCLEINPC LENHGGCDKNAECTQTGPNQ AACNCLPAYTGDGKVCTLIN
rHARE  322 CAAGFRGNGTVCTAINACET SNGGCSTKADCKRTTPGNRV CVCKAGYTGDGIVCLEINPC LENHGGCDRNAECTQTGPNQ AVCNCLPKYTGDGKVCSLIN

hHARE  401 VCLTKNGGCSEFAICNHT Q VERTCTCKPNYIGDGFTCRG SIYQELPKNPKTSQYFFQLQ EHFVKDLVGPGPFTVFAPLS AAFDEEARVKDWDKYGLMPQ
rHARE  422 VCLTNNGGCSPFAFCNYT Q DQRICTCKPDYTGDGIVCRG SIYGELPKNPSTSQYFFQLQ EHAVRELAGPGPFTVFAPLS SSFNHEPRIKDWDQQGLMSQ

hHARE  501 VLRYHVVACHQLLLENLKLI SNATSLQGEPIVISVSQSTV YINNKAKIISSDIISTNGIV HIIDKLLSPKNLLITPKDNS GRILQNLTTLATNNGYIKFS
rHARE  522 VLRYHVVGCQQLLLDNLKVT TSATTLQGEPVSISVSQDTV FINNEAKVLSSDIISTNGVI HVIDKLLSPKNLLITPKDAL GRVLQNLTTVAANHGYTKFS

hHARE  601 NLIQDSGLLSVITDPIHTPV TLFWPTDQALHALPAEQQDF LFNQDNKDKLKEYLKFHVIR DAKVLAVDLPTSTAWKTLQG SELSVKCGAGRDIGDLFLNG
rHARE  622 KLIQDSGLLSVITDSIHTPV TVFWPTDKALEALPPEQQDF LFNQDNKDKLKSYLKFHVIR DSKALASDLPRSASWKTLQG SELSVRCGTGSDIGELFLNE

hHARE  701 QTCRIVQRELLFDLGVAYGI DCLLIDPTLGGRCDTFTTFD ASGECGSCVNTPSCPRWSKP KGVKQKCLYN-LPFKRNLEG CRERCSLVIQIPRCCKGYFG
rHARE  722 QMCRFIHRGLLFDVGVAYGI DCLLMNPTLGGRCDTFTTFD IPGECGSCIFTPKCPLKSKP KGVKKKCIYNPLPFRRNVEG CQNLCTVVIQTPRCCHGYFM

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rHARE  822 PDCQACPGGPDTPCNNRGMC RDLYTPMGQCLCHTGFNGTA CELCWHGRFGPDCQPRSCSE HGQCDEGITGSGECLCETGW TAASCDTPTAVFAVCTPACS

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rHARE  922 VHATCTENNTCVCNLNYEGD GITCTVVDFCKQNNGGCAKV AKCSQKGTQVSCSCKKGYKG DGYSCIEIDPCADGVNGGCH EHATCRMTGPGKHKCECKSH

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rHARE 1022 YVGDGVDCEPEQLPLDRCLQ DNGQCHPDASCADLYFQDTT VGVFHLRSPLGQYKLTFDKA KEACAKEAATIATYNQLSYA QKAKYHLCSAGWLESGRVAY

hHARE 1100 PTAFASQNCGSGVVGIVDYG PRPNKSEMWDVFCYRMKDVN CTCKVGYVGDGFSCSGNLLQ VLMSFPSLTNFLTEVLAYSN SSARGRAFLEHLTDLSIRGT
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rHARE 1321 HSGLGTGIFCAVVLVTGAIA LAAYSYFRLKQRTTGFQRFD QKRTLMSWLLASSSPRISQT LCMRPQRRHPQSPPVTPSQT LENRIWRTATLWGHCGPDMR

rHARE 1421 SQQATTVTVPR
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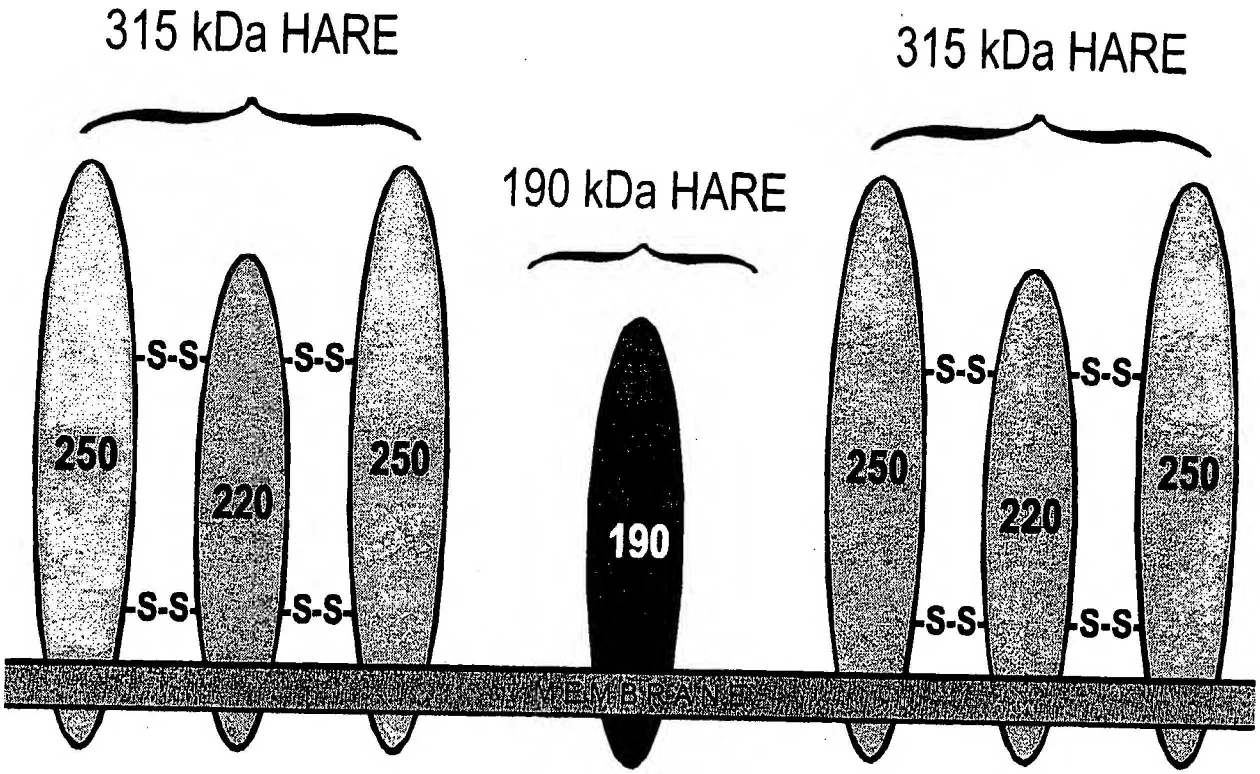
Figure 36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190 kDa HARE
315 kDa HARE
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220
250
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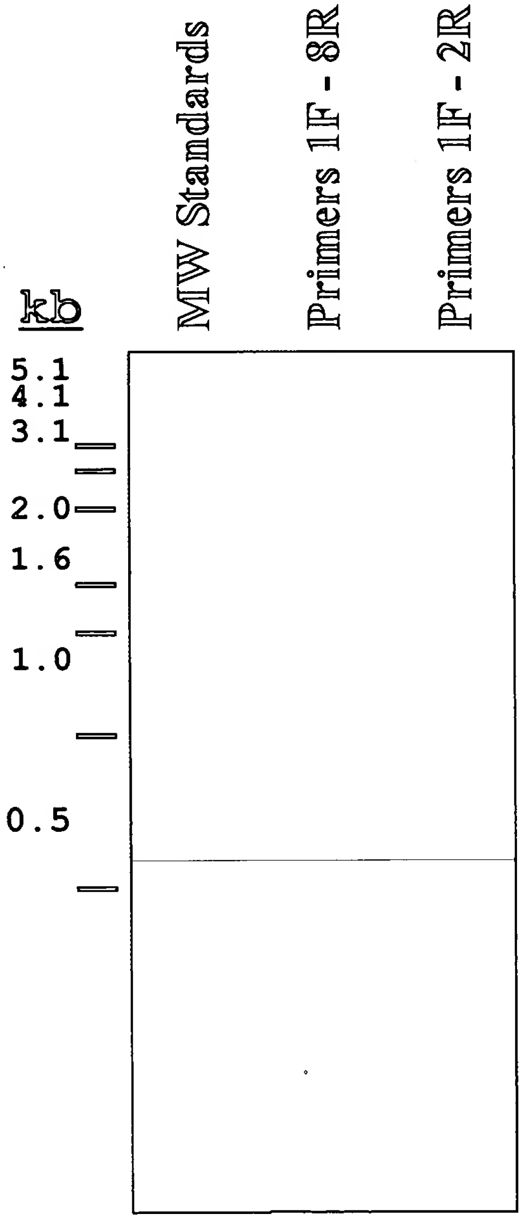
-S-S-
-S-S-
-S-S-
190
250
220
250
-S-S-
-S-S-
-S-S-
-S-S-
MEMBRANE

Figure 37

Amplification of the 1394 amino acid HARE Open Reading Frame from a human lymph node cDNA Llibrary


kb
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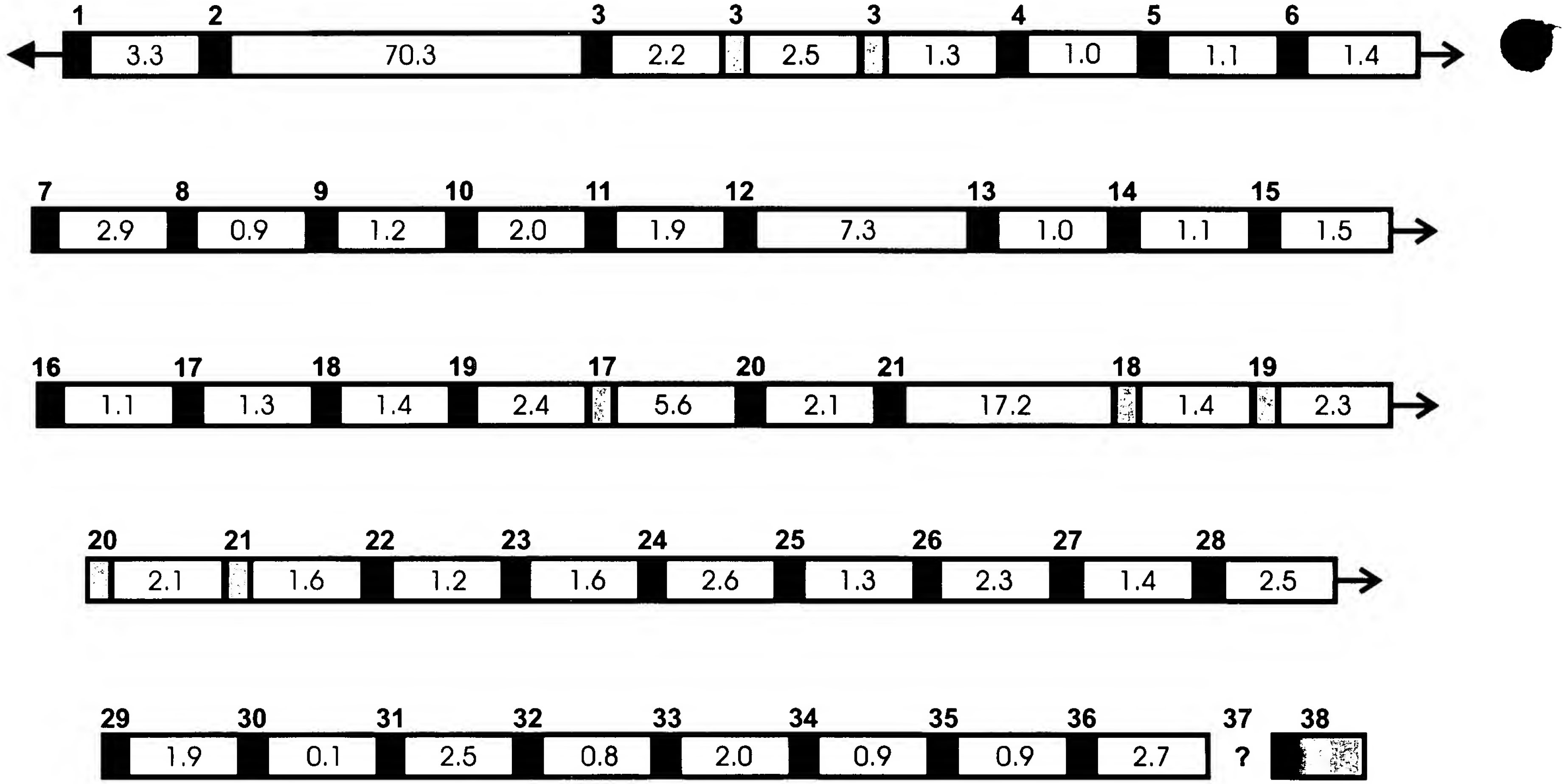
4.1
3.1
2.0
1.6
1.0
0.5
MW Standards
Primers 1F - 8R
Primers 1F - 2R

Figure 38

Schematic Organization of the Human HARE Gene on Chromosome 12
(encoding 1357 of the 1394 amino acids disclosed here)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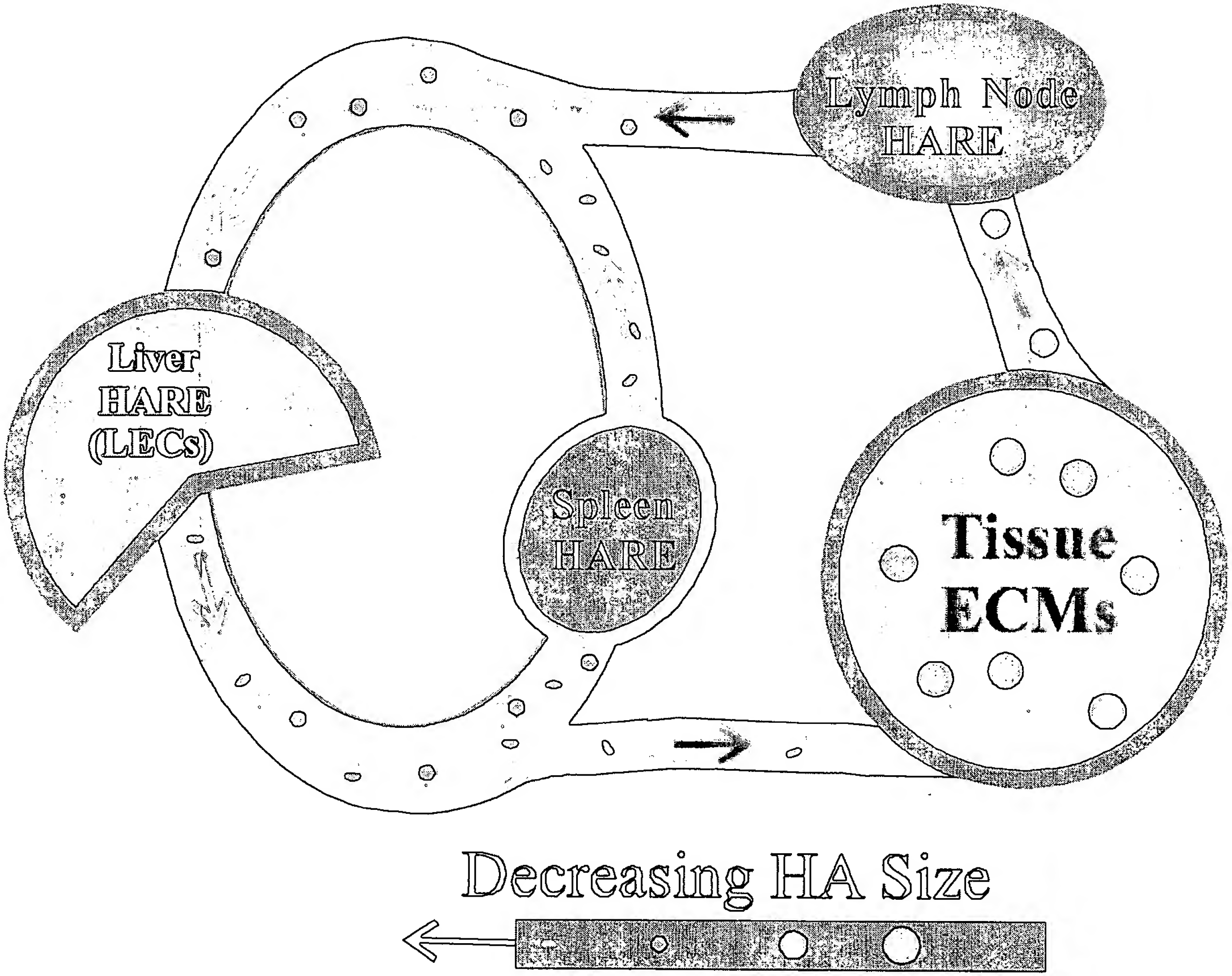
2.7
?

Figure 3 9


Liver
HARE
(LECs)
Lymph Node
HARE
Spleen
HARE
Tissue
ECMs
Decreasing HA Size